

10/524983

21078WO.ST25.txt

SEQUENCE LISTING

<110> DSM IP Assets B.V.

<120> NOVEL LIPASES AND USES THEREOF

<130> 21078WO

<160> 39

<170> PatentIn version 3.1

<210> 1

<211> 3728

<212> DNA

<213> Aspergillus niger.

<400> 1

cgggcaatta	cgatccgagc	gcgctatcta	cgtgcaccgg	aagcttgctc	cttgatttgt	60
tgtttcataa	tacttatttg	tgctcttttag	cccgactgca	gtggtggctg	catgttgggc	120
aggtatttaa	ctttgggcga	taccaactac	gcgtgcactt	tgaagcatag	cacggcgcgc	180
cggggatgcg	tgctcgtcta	tgactataat	tgatgtggcc	gactgactgc	ttggtgttag	240
ggatcttggtg	tttatcttgg	ttttctgtac	ttagaagaga	gtgccggtgg	catggtgggc	300
gatataacta	gagcaatgcg	tgtctccatc	ctcatcctca	tccggccatcc	cttataccct	360
gatggcgccg	aaggggtgaga	atggcgaatg	gcgagaataa	tatactgtgt	atagtctgtc	420
ctatcctcct	tgtgcactgc	aaagtcagtt	gatcatcatc	cccactcaat	cgtccactca	480
tgctctatat	ccgagacaaa	ccacaactta	ttcaatttaa	gcccagatcc	ataatcatcc	540
acaaccaccc	cacagccagg	gtacatccag	ggtctctttc	ccgccggaga	aactaagccc	600
ttagctcctc	actaggacct	cccgcgcgct	cttggtcctc	catcaccaac	tttccaccta	660
taaactgcat	caaacatgct	gcaaagccac	gactgctgct	gcatgcaccc	caacatcatc	720
cccgcataat	acatccatcc	ctgaagcaat	caagcttgac	tctgttggtt	cttcggagat	780
gttaaccatt	cgtactttcc	aaatgacatc	aatccaactg	atagacatcg	ccatcctcct	840
caataccatg	gacgccccac	gtccatgtca	aaagtaagac	tagctcagct	cggcggttaat	900
caattatgat	tgcgagtctc	aatccctgag	tcatgtgttc	tctgtgtcgg	agaattagac	960
tgaattcagc	tgctcgttgc	cactcctagc	tccctgataa	aggtcctcac	ttcgtctcgt	1020
agctggctgg	ctgcatattc	tccggtgact	aagttaacag	aaccagcaac	ttagtagcca	1080
tggcgagcgc	actcctctgg	ctctcccctgc	tgggtggcag	caccctagcc	tcaactctag	1140
acaccagtaa	tacccttacc	atcaagagag	cagacgcagg	aaacaacacc	tcctcaatcc	1200
caacagccac	cctcaacaac	accgtcttca	tccggcgttc	cctgcccagag	ttcgagcagg	1260
agttgttcct	gggtatcaag	tttgctgatg	agcccgtgcg	attcaccccg	tcgacgttga	1320
aaaccgtcta	tcgcgccaat	gacagcgaca	acggggtgta	tcatgcttcc	acagcatccg	1380
gactgcagac	ttcctcgggg	accgtgctct	acaacgccac	agagtatggg	tatgattgcc	1440
ccgggtatgg	atccgatgag	acggagctgg	cggaggaagg	atatgcgcgg	ttcgatgaga	1500

21078W0.ST25.txt

actgtatgaa	cctgaatata	attcggccca	agagagagaa	agaggatgag	ttgttgcctg	1560
tgatgatttg	gatctttggt	ggtggttggg	tgagggtgc	gactgctgat	ccgaggtagg	1620
atactatagt	tttgtgctgt	gctgtgtggg	gttgatgctg	acgatgtgca	aggtacaata	1680
tgagctatat	tgttcgccag	ggtgcttga	atgataagcc	tgtcttgggt	gtctcgatca	1740
attaccgtgt	ggctgcgttt	ggattccttg	actctgtcga	ggttatggtg	cgtttcttcc	1800
ttcaccgtca	agtatatggg	tttcagctga	catgacatct	gtaggaatcc	ggcaacacga	1860
acctaggact	tcgtgatcag	cgctgcgcca	tgattggtg	caaacaaaac	atcaaggcgt	1920
ttggtggtga	cccggacaag	atcaccatct	ggggagaatc	agcgtgagat	tataccctaa	1980
tagcattcga	tatacagcgc	ctgacatggc	acagtgggtc	ctacagcgtc	ggagcccacc	2040
tggtcaccaa	cgacggtgac	aacgaggggc	tattcagagc	cggtatgcac	accactcccc	2100
aattctcgtc	tcctcatctg	ctaaccagca	tagccatcat	ggaatccggc	aacgcagtcg	2160
gaccccccta	caacggcacg	gactggtacc	agccgatgta	cgaccagatc	gtgaacgcaa	2220
ccaagtatgt	cctcaccttc	cccaaaagac	aatactcaaa	tgactagtat	atatactaac	2280
tacatgaaag	ctgcaccacc	tcaagcaaca	cccttcaatg	cctccgcgaa	gtcccccttct	2340
caacgatcta	caccgccgca	gacatcggcc	tggaatggtt	cgccaccatc	gacggcacct	2400
tcataaaaga	atatccccaa	atcagcatta	cggagggccg	cttcgccaag	gtccccatcc	2460
tccatggcac	caacaccgac	gagggcggtga	gtttcggtag	gacgggcgtg	aacactgatg	2520
ccgaagcgat	ccagcagttg	atgggtgagc	ccccccccc	cccccttccc	accaatcccc	2580
aagatatata	tatagtacga	gatactaagg	tgaaatgaaa	atgatagcat	ccaaacgctg	2640
ggctcctaaac	gaaacccaag	ccacgaccct	cctatcgac	tatcccaaca	tctccgccct	2700
aggctgtccc	tacggatggg	gcaacacgac	ctggccgaag	ctggggtatg	aatataagcg	2760
ctacgagtcg	atggcgggcg	atctgtgcat	ggttgctccg	aggagggtgc	tcagtcagaa	2820
gatgaaggag	tatgaggagc	aagtgtttgc	gtatcggtgg	gatgtcgctg	cgttgaatga	2880
ttcgagtacg	attgggggtg	cgcattttgc	tgaggtaatg	ccatccatcc	atcccctatt	2940
attggttttc	cctgcggtat	gatatttggg	atgctaata	tgtgttactg	cgtgcatgca	3000
tagatcccg	ttgttttcgc	caaccctgtg	cagaacatca	ctccgttggg	aagtgatccc	3060
gcaagactgg	agttgggtga	tctggccgcg	aggatgtgga	cggcttttgt	gacggatttg	3120
gatccgaatg	ggcatggtgg	tacgttcctc	ttctccatct	tattagaatt	gtgaaatgaa	3180
gcgtgtggtt	ctaatagggg	tgacagtctc	tggtatcccc	cactggccga	aatacaacct	3240
cactgatccg	agggactttg	tgttccggct	accgagggat	ggaagttagt	tgagagaagga	3300
tacttttagg	acggggggga	ttgattatat	taatacaatt	gtgcggtaag	ttgctgctaa	3360
gtagtactac	tatatgtata	taggaggggtg	tggtgaaaa	gtagatagta	gtactatata	3420
aaggatggtt	agatactata	tactattttac	tactactgta	atgttactat	aatcaagact	3480
agaagaaagt	ctactgattg	attacttcga	ctgatcgatt	gtattgatct	agttagtata	3540
tcaaatcgac	aaagagccgc	cgtttttatt	cattcatatt	tcccgccact	aagccagtat	3600
actataccat	agtagtatag	ctggtttagt	tgatgccgag	cagctcaacc	tcgctaattg	3660
atatcagcat	tccaatccat	tttttactg	gcaaagaata	ttagaagagg	aaggaggagg	3720
aggataac						3728

<210> 2

<211> 1749

<212> DNA

<213> *Aspergillus niger*

21078WO.ST25.txt

<220>

<221> CDS

<222> (1)..(1749)

<400> 2

atg gcg agc gca ctc ctc tgg ctc tcc ctg ctg ggt ggc agc acc cta	48
Met Ala Ser Ala Leu Leu Trp Leu Ser Leu Leu Gly Gly Ser Thr Leu	
1 5 10 15	
gcc tca act cta gac acc agt aat acc cct acc atc aag aga gca gac	96
Ala Ser Thr Leu Asp Thr Ser Asn Thr Pro Thr Ile Lys Arg Ala Asp	
20 25 30	
gca gga aac aac acc tcc tca atc cca aca gcc acc ctc aac aac acc	144
Ala Gly Asn Asn Thr Ser Ser Ile Pro Thr Ala Thr Leu Asn Asn Thr	
35 40 45	
gtc ttc atc ggc cgt tcc ctg ccc gag ttc gag cag gag ttg ttc ctg	192
Val Phe Ile Gly Arg Ser Leu Pro Glu Phe Glu Gln Glu Leu Phe Leu	
50 55 60	
ggc atc aag ttt gct gat gag ccc gtg cga ttc acc ccg tcg acg ttg	240
Gly Ile Lys Phe Ala Asp Glu Pro Val Arg Phe Thr Pro Ser Thr Leu	
65 70 75 80	
aaa acc gtc tat cgc gcc aat gac agc gac aac ggg gtg tat cat gct	288
Lys Thr Val Tyr Arg Ala Asn Asp Ser Asp Asn Gly Val Tyr His Ala	
85 90 95	
tcc aca gca tcc gga ctg cag act tcc tcg ggg acc gtg ctc tac aac	336
Ser Thr Ala Ser Gly Leu Gln Thr Ser Ser Gly Thr Val Leu Tyr Asn	
100 105 110	
gcc aca gag tat ggg tat gat tgc ccc ggg tat gga tcc gat gag acg	384
Ala Thr Glu Tyr Gly Tyr Asp Cys Pro Gly Tyr Gly Ser Asp Glu Thr	
115 120 125	
gag ctg gcg gag gaa gga tat gcg cgg ttc gat gag aac tgt atg aac	432
Glu Leu Ala Glu Glu Gly Tyr Ala Arg Phe Asp Glu Asn Cys Met Asn	
130 135 140	
ctg aat ata att cgg ccc aag aga gag aaa gag gat gag ttg ttg cct	480
Leu Asn Ile Ile Arg Pro Lys Arg Glu Lys Glu Asp Glu Leu Leu Pro	
145 150 155 160	
gtg atg att tgg atc ttt ggt ggt ggt tgg gtg cag ggt gcg act gct	528
Val Met Ile Trp Ile Phe Gly Gly Gly Trp Val Gln Gly Ala Thr Ala	
165 170 175	
gat ccg agg tac aat atg agc tat att gtt cgc cag ggt gcg ttg aat	576
Asp Pro Arg Tyr Asn Met Ser Tyr Ile Val Arg Gln Gly Ala Leu Asn	
180 185 190	
gat aag cct gtc ttg ggt gtc tcg atc aat tac cgt gtg gct gcg ttt	624
Asp Lys Pro Val Leu Gly Val Ser Ile Asn Tyr Arg Val Ala Ala Phe	

21078WO.ST25.txt

195	200	205	
gga ttc ctt gac tct gtc gag gtt atg gaa tcc ggc aac acg aac cta			672
Gly Phe Leu Asp Ser Val Glu Val Met Glu Ser Gly Asn Thr Asn Leu			
210	215	220	
gga ctt cgt gat cag cgc gtc gcc atg cat tgg gtc aaa caa aac atc			720
Gly Leu Arg Asp Gln Arg Val Ala Met His Trp Val Lys Gln Asn Ile			
225	230	235	240
aag gcg ttt ggt ggt gac ccg gac aag atc acc atc tgg gga gaa tca			768
Lys Ala Phe Gly Gly Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser			
245	250	255	
gct ggt gcc tac agc gtc gga gcc cac ctg gtc acc aac gac ggt gac			816
Ala Gly Ala Tyr Ser Val Gly Ala His Leu Val Thr Asn Asp Gly Asp			
260	265	270	
aac gag ggt cta ttc aga gcc gcc atc atg gaa tcc ggc aac gca gtc			864
Asn Glu Gly Leu Phe Arg Ala Ala Ile Met Glu Ser Gly Asn Ala Val			
275	280	285	
gga ccc ccc tac aac ggc acg gac tgg tac cag ccg atg tac gac cag			912
Gly Pro Pro Tyr Asn Gly Thr Asp Trp Tyr Gln Pro Met Tyr Asp Gln			
290	295	300	
atc gtg aac gca acc aac tgc acc acc tca agc aac acc ctt caa tgc			960
Ile Val Asn Ala Thr Asn Cys Thr Thr Ser Ser Asn Thr Leu Gln Cys			
305	310	315	320
ctc cgc gaa gtc ccc ttc tca acg atc tac acc gcc gca gac atc ggc			1008
Leu Arg Glu Val Pro Phe Ser Thr Ile Tyr Thr Ala Ala Asp Ile Gly			
325	330	335	
ctg gaa tgg ttc gcc acc atc gac ggc acc ttc atc aaa gaa tat ccc			1056
Leu Glu Trp Phe Ala Thr Ile Asp Gly Thr Phe Ile Lys Glu Tyr Pro			
340	345	350	
caa atc agc att acg gag ggc cgc ttc gcc aag gtc ccc atc ctc cat			1104
Gln Ile Ser Ile Thr Glu Gly Arg Phe Ala Lys Val Pro Ile Leu His			
355	360	365	
ggc acc aac acc gac gag ggc gtg agt ttc ggt acg acg ggc gtg aac			1152
Gly Thr Asn Thr Asp Glu Gly Val Ser Phe Gly Thr Thr Gly Val Asn			
370	375	380	
act gat gcc gaa gcg atc cag cag ttg atg gca tcc aaa cgc tgg gtc			1200
Thr Asp Ala Glu Ala Ile Gln Gln Leu Met Ala Ser Lys Arg Trp Val			
385	390	395	400
cta aac gaa acc caa gcc acg acc ctc cta tcg cac tat ccc aac atc			1248
Leu Asn Glu Thr Gln Ala Thr Thr Leu Leu Ser His Tyr Pro Asn Ile			
405	410	415	
tcc gcc cta ggc tgt ccc tac gga tgg ggc aac acg acc tgg ccg aag			1296
Ser Ala Leu Gly Cys Pro Tyr Gly Trp Gly Asn Thr Thr Trp Pro Lys			
420	425	430	
ctg ggg tat gaa tat aag cgc tac gag tcg atg gcg ggc gat ctg tgc			1344

21078WO.ST25.txt

Leu Gly Tyr Glu Tyr Lys Arg Tyr Glu Ser Met Ala Gly Asp Leu Cys
 435 440 445
 atg gtt gct ccg agg agg ttg ctc agt cag aag atg aag gag tat gag 1392
 Met Val Ala Pro Arg Arg Leu Leu Ser Gln Lys Met Lys Glu Tyr Glu
 450 455 460
 gag caa gtg ttt gcg tat cgg tgg gat gtc gct gcg ttg aat gat tcg 1440
 Glu Gln Val Phe Ala Tyr Arg Trp Asp Val Ala Ala Leu Asn Asp Ser
 465 470 475 480
 agt acg att ggg gtg gcg cat ttt gct gag atc ccg ttt gtt ttc gcc 1488
 Ser Thr Ile Gly Val Ala His Phe Ala Glu Ile Pro Phe Val Phe Ala
 485 490 495
 aac cct gtg cag aac atc act ccg ttg gga agt gat ccc gca aga ctg 1536
 Asn Pro Val Gln Asn Ile Thr Pro Leu Gly Ser Asp Pro Ala Arg Leu
 500 505 510
 gag ttg ggt aat ctg gcc gcg agg atg tgg acg gct ttt gtg acg gat 1584
 Glu Leu Gly Asn Leu Ala Ala Arg Met Trp Thr Ala Phe Val Thr Asp
 515 520 525
 ttg gat ccg aat ggg cat ggt gtc tct ggt atc ccc cac tgg ccg aaa 1632
 Leu Asp Pro Asn Gly His Gly Val Ser Gly Ile Pro His Trp Pro Lys
 530 535 540
 tac aac ctc act gat ccg agg gac ttt gtg ttc cgg cta ccg agg gat 1680
 Tyr Asn Leu Thr Asp Pro Arg Asp Phe Val Phe Arg Leu Pro Arg Asp
 545 550 555 560
 gga agt tat gtg gag aag gat act ttt agg acg ggg ggg att gat tat 1728
 Gly Ser Tyr Val Glu Lys Asp Thr Phe Arg Thr Gly Gly Ile Asp Tyr
 565 570 575
 att aat aca att gtg ccg taa 1749
 Ile Asn Thr Ile Val Arg
 580

<210> 3

<211> 582

<212> PRT

<213> *Aspergillus niger*

<400> 3

Met Ala Ser Ala Leu Leu Trp Leu Ser Leu Leu Gly Gly Ser Thr Leu
 1 5 10 15
 Ala Ser Thr Leu Asp Thr Ser Asn Thr Pro Thr Ile Lys Arg Ala Asp
 20 25 30
 Ala Gly Asn Asn Thr Ser Ser Ile Pro Thr Ala Thr Leu Asn Asn Thr
 35 40 45
 Val Phe Ile Gly Arg Ser Leu Pro Glu Phe Glu Gln Glu Leu Phe Leu

21078WO.ST25.txt

50 55 60
 Gly Ile Lys Phe Ala Asp Glu Pro Val Arg Phe Thr Pro Ser Thr Leu
 65 70 75 80
 Lys Thr Val Tyr Arg Ala Asn Asp Ser Asp Asn Gly Val Tyr His Ala
 85 90 95
 Ser Thr Ala Ser Gly Leu Gln Thr Ser Ser Gly Thr Val Leu Tyr Asn
 100 105 110
 Ala Thr Glu Tyr Gly Tyr Asp Cys Pro Gly Tyr Gly Ser Asp Glu Thr
 115 120 125
 Glu Leu Ala Glu Glu Gly Tyr Ala Arg Phe Asp Glu Asn Cys Met Asn
 130 135 140
 Leu Asn Ile Ile Arg Pro Lys Arg Glu Lys Glu Asp Glu Leu Leu Pro
 145 150 155 160
 Val Met Ile Trp Ile Phe Gly Gly Gly Trp Val Gln Gly Ala Thr Ala
 165 170 175
 Asp Pro Arg Tyr Asn Met Ser Tyr Ile Val Arg Gln Gly Ala Leu Asn
 180 185 190
 Asp Lys Pro Val Leu Gly Val Ser Ile Asn Tyr Arg Val Ala Ala Phe
 195 200 205
 Gly Phe Leu Asp Ser Val Glu Val Met Glu Ser Gly Asn Thr Asn Leu
 210 215 220
 Gly Leu Arg Asp Gln Arg Val Ala Met His Trp Val Lys Gln Asn Ile
 225 230 235 240
 Lys Ala Phe Gly Gly Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser
 245 250 255
 Ala Gly Ala Tyr Ser Val Gly Ala His Leu Val Thr Asn Asp Gly Asp
 260 265 270
 Asn Glu Gly Leu Phe Arg Ala Ala Ile Met Glu Ser Gly Asn Ala Val
 275 280 285
 Gly Pro Pro Tyr Asn Gly Thr Asp Trp Tyr Gln Pro Met Tyr Asp Gln
 290 295 300
 Ile Val Asn Ala Thr Asn Cys Thr Thr Ser Ser Asn Thr Leu Gln Cys
 305 310 315 320
 Leu Arg Glu Val Pro Phe Ser Thr Ile Tyr Thr Ala Ala Asp Ile Gly
 325 330 335
 Leu Glu Trp Phe Ala Thr Ile Asp Gly Thr Phe Ile Lys Glu Tyr Pro
 340 345 350
 Gln Ile Ser Ile Thr Glu Gly Arg Phe Ala Lys Val Pro Ile Leu His
 355 360 365
 Gly Thr Asn Thr Asp Glu Gly Val Ser Phe Gly Thr Thr Gly Val Asn
 370 375 380
 Thr Asp Ala Glu Ala Ile Gln Gln Leu Met Ala Ser Lys Arg Trp Val
 385 390 395 400
 Leu Asn Glu Thr Gln Ala Thr Thr Leu Leu Ser His Tyr Pro Asn Ile

21078WO.ST25.txt

	405		410		415										
Ser	Ala	Leu	Gly	Cys	Pro	Tyr	Gly	Trp	Gly	Asn	Thr	Thr	Trp	Pro	Lys
	420		425		430										
Leu	Gly	Tyr	Glu	Tyr	Lys	Arg	Tyr	Glu	Ser	Met	Ala	Gly	Asp	Leu	Cys
	435		440		445										
Met	Val	Ala	Pro	Arg	Arg	Leu	Leu	Ser	Gln	Lys	Met	Lys	Glu	Tyr	Glu
	450		455		460										
Glu	Gln	Val	Phe	Ala	Tyr	Arg	Trp	Asp	Val	Ala	Ala	Leu	Asn	Asp	Ser
465			470		475									480	
Ser	Thr	Ile	Gly	Val	Ala	His	Phe	Ala	Glu	Ile	Pro	Phe	Val	Phe	Ala
	485		490		495										
Asn	Pro	Val	Gln	Asn	Ile	Thr	Pro	Leu	Gly	Ser	Asp	Pro	Ala	Arg	Leu
	500		505		510										
Glu	Leu	Gly	Asn	Leu	Ala	Ala	Arg	Met	Trp	Thr	Ala	Phe	Val	Thr	Asp
	515		520		525										
Leu	Asp	Pro	Asn	Gly	His	Gly	Val	Ser	Gly	Ile	Pro	His	Trp	Pro	Lys
	530		535		540										
Tyr	Asn	Leu	Thr	Asp	Pro	Arg	Asp	Phe	Val	Phe	Arg	Leu	Pro	Arg	Asp
545			550		555									560	
Gly	Ser	Tyr	Val	Glu	Lys	Asp	Thr	Phe	Arg	Thr	Gly	Gly	Ile	Asp	Tyr
	565		570		575										
Ile	Asn	Thr	Ile	Val	Arg										
	580														

<210> 4

<211> 3853

<212> DNA

<213> Aspergillus niger

<400> 4

ctttcctggt	gcccgggtctt	tggtggtgtc	ataggataca	attaccaga	caacgttcgg	60
tttgtcgatc	agttttaagt	gtgcgtggac	tgacagccaa	ggccactggg	gcccctgcct	120
ctatcattta	attccacacg	ctcgcctctg	cagctctggc	accagcgttg	caaattccag	180
gggtcagcct	acgtggcatt	aggctctaag	agaatctgag	ggaaaggatt	tcacttagaa	240
aaatttatcg	gtccggcttg	tccgatcggg	aggaaggcat	tgcttcccct	catatgcggc	300
cccggttccc	aagcagctga	ttcgggacgt	tttccggctt	gatcgctata	ctctcataat	360
ctctcctgca	agagctggat	aaacttggtt	tcttatcttc	cgtggggatg	ccatagtcca	420
gtagacgctg	tctcgaaatt	gagtagcacc	actatttacg	ggcaagttaa	tggcacatgt	480
attagctttg	tactgacggt	tgaaatgtgg	agcaatttcc	ggctatgtac	cggatctggt	540
ccgatatctt	tcatcgcaat	tagttagtac	ataaaactcc	ctagtcacgc	aagaacggtt	600
cgaacataac	gaattaaaaa	ttctcattct	ctggcaaggc	ttcgaaatgt	ttgtttcctc	660
gcttgctcta	ttagcactta	ttgctccttt	gatcgcaatt	gcggtaaaaa	tagaacagcc	720
aggaataaat	ccaaatccca	cagctactgt	acgaaatggc	acctactatg	gtctccataa	780

21078W0.ST25.txt

ccagcactat	aatcaagacc	tctttctcgg	tattccatat	gcacagcaac	ctattggtga	840
ccttcgcttg	cggacccac	gatcaatgaa	cacctcctgg	ccagtaccaa	gaaatgcaac	900
agaatattca	cccgcattgt	ttggatttaa	tcagacagag	ggtgcttccg	aagcctgcct	960
tactctcaat	gtcgtccgcc	cggcaagcat	cgctctttct	gaaagtcttc	ccgttgctgg	1020
tcagtatata	ccccaaatct	gatcagaagg	gccagaactg	actttgcgct	cggccccagt	1080
ctggattcat	ggcgggggat	tcacctccgg	ctcttcatca	gagaaacaat	acaatctgtc	1140
cttcatcggt	gatcagtcag	tccaaatgga	aaagcccgtt	atcgcagtca	gtctaaatta	1200
tcgtcttcaa	tgctgggggt	ttatgtggag	caaggagatg	aaggaagccg	gagtagggaa	1260
cctgggactt	agagaccaac	gattagctct	gcattggata	caagaaagta	ggtatctcga	1320
tagtgaagct	cttccaagta	cggatctgac	catgacttag	acattgctgc	gtttggtgga	1380
gaccctgctc	aggttacaat	ttgggggtgaa	agtgccggcg	ctaatagtgt	tggcacacat	1440
ctggttgctt	acggagggcg	cgatgatggg	atattccgtg	cagctatcag	tgaaagtggg	1500
gccccaaagt	tttaccacg	ttatccaaca	cctgctgaat	ggcagcccta	ttatgatggg	1560
attgtgaatg	catcaggctg	cagttcagca	acggatactt	tggcttgtct	ccgaacaatt	1620
ccaactaaca	tattgcatgg	catctttgac	aacacgtcta	ttgtacccat	gcacgctatt	1680
tcaggcctca	gcggagcaaa	attcattcct	gtcatagatg	acgacttcat	taaagagagt	1740
gccacgggtc	agctccagaa	gggcaacttc	gtcaaagttc	cctacttgat	tggagctaac	1800
gccgacgaag	ggactgcatt	tgctgtggag	ggagtcaaca	cagatgctga	gtttcgcgag	1860
ctagtcaaa	gttggggcct	caacaacgct	accacggata	tcttgaggcg	cctataacca	1920
gacattcctc	agataggaat	ccccgccata	atgggttgaa	ggccaccgtc	cggatatgga	1980
aatcaataca	agcgtgtggc	cgcatttcag	ggtgatgtta	acatccatgc	cgcacgtagg	2040
ttgaccagtc	agatctggtc	atccccgaat	atctcagtat	atagctacat	gtttgacggt	2100
atcagccctg	gatatggccc	ctctgctggg	tcctatgctg	gggctactca	tggtagctat	2160
attccgtacg	ttttctataa	tctggatggc	ctgggggatg	actcgaacaa	caagtccata	2220
gaaagcatac	ctaacagtta	ttccccgatg	agcaaaatta	tgtcaagaat	gtgggtcagt	2280
tttgtgacaa	cattggaccc	aaatcattct	ggagggtatg	tcccacatcc	cattcctatg	2340
attgcgcaat	gtcagaccg	agctgaatca	actatcttct	taggaactaa	tgttcagtgg	2400
ccgccataca	atatcgataa	tccggagata	atctttttcg	ataccgatgt	cacgaacctc	2460
acatatgtga	gttctgacgt	ttaccgtgcg	gagggcataa	aatacatcag	tgatcacctt	2520
gcaagtgatt	tcgggcactg	agatcacata	tcttctcggg	ctaatttttag	aatgactgtg	2580
gtctcatcta	accagacttg	gcccgcaggt	ctttacgccc	actggtggta	attgatgcaa	2640
cccccaagct	atatagtgtc	tggggctttg	aactactgtc	aatgagcgaa	aattgactat	2700
ttccctttat	gactcatgta	gtagcatttg	tgctggcact	gtgatcaaga	tatgtttttc	2760
gagattaccg	gtagcagagt	agtcgatgtc	gccaatatta	ttcatctata	atgaatagta	2820
ataacttagg	agtcattcag	tatagtcgat	actgacataa	gtatcttttc	ttgtgatatt	2880
tataatatgt	cccgtttggc	cttgtttgta	gtaactctca	tagcctgctg	cttgagaact	2940
catctgttca	atcatagaga	taccaattat	ggaaggatag	gttggcatcg	gtgtttgttt	3000
catcaagact	actacctaata	aagtcactga	agaaggctgt	agactgaaag	cgcgacattg	3060
atgattagaa	ttccaacttt	ggtcaacata	tgcattagac	tataaaaggg	acatgttaga	3120
agaactaagt	acatacgacc	ataggggtgtg	gaaaacaggg	cttcccgtcc	gctcagccgt	3180
acttaagcca	cacgccggga	ggttagtagt	tgggtgggtg	accaccagcg	aatcccttct	3240
gttgatgttt	tttgtttctc	tataaaactt	ttgggtcggg	atctcgagat	gtcttccagg	3300
atgctaaaac	cttcgggttc	ctcacagcgg	agatgggtgtc	aactggcttt	tttaatgcat	3360
tcttggctaa	agtgctcgtg	aacacggcaa	tatagtacga	tgatatctga	agtttgtggg	3420

21078W0.ST25.txt

gtcaagacat atgcttattg tgaccaccag accataaatc ggagtattca cagcttatat	3480
catcctcaaa cattgattgc atagtagagt gtctaactct tgactcaagg gattgaaaaat	3540
gattattttga aaatataggt agttttgaat aacattctgg cacacgagct ttagctggat	3600
tagtaagatg tgacgccgat tttgggtttg attatgtcat catttggcag ttccccaga	3660
ggacagcccg gttaagaacg aaccttttct gagcccgat acaaatgcgg ggaacagaga	3720
tgaggagatg ccgaagcatg ctttggcaaa cagaagccac tgtgaaaaac cattcacaga	3780
tatcttgtga tagttggatt gcactgactg tccgcgaaag cgagcatatc tatcccgat	3840
actgagaact agt	3853

<210> 5

<211> 1743

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1743)

<400> 5

atg ttt gtt tcc tcg ctt gct cta tta gca ctt att gct cct ttg atc	48
Met Phe Val Ser Ser Leu Ala Leu Leu Ala Leu Ile Ala Pro Leu Ile	
1 5 10 15	
gca att gcg gta aaa ata gaa cag cca gga ata aat cca aat ccc aca	96
Ala Ile Ala Val Lys Ile Glu Gln Pro Gly Ile Asn Pro Asn Pro Thr	
20 25 30	
gct act gta cga aat ggc acc tac tat ggt ctc cat aac cag cac tat	144
Ala Thr Val Arg Asn Gly Thr Tyr Tyr Gly Leu His Asn Gln His Tyr	
35 40 45	
aat caa gac ctc ttt ctc ggt att cca tat gca cag caa cct att ggt	192
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Gln Pro Ile Gly	
50 55 60	
gac ctt cgc ttg cgg acc cca cga tca atg aac acc tcc tgg cca gta	240
Asp Leu Arg Leu Arg Thr Pro Arg Ser Met Asn Thr Ser Trp Pro Val	
65 70 75 80	
cca aga aat gca aca gaa tat tca ccc gca tgt gtt gga ttt aat cag	288
Pro Arg Asn Ala Thr Glu Tyr Ser Pro Ala Cys Val Gly Phe Asn Gln	
85 90 95	
aca gag ggt gct tcc gaa gcc tgc ctt act ctc aat gtc gtc cgc ccg	336
Thr Glu Gly Ala Ser Glu Ala Cys Leu Thr Leu Asn Val Val Arg Pro	
100 105 110	
gca agc atc gct ctt tct gaa agt ctt ccc gtt gct gtc tgg att cat	384
Ala Ser Ile Ala Leu Ser Glu Ser Leu Pro Val Ala Val Trp Ile His	
115 120 125	

21078WO.ST25.txt

ggc ggg gga ttc acc tcc ggc tct tca tca gag aaa caa tac aat ctg	432
Gly Gly Gly Phe Thr Ser Gly Ser Ser Ser Glu Lys Gln Tyr Asn Leu	
130 135 140	
tcc ttc atc gtt gat cag tca gtc caa atg gaa aag ccc gtt atc gca	480
Ser Phe Ile Val Asp Gln Ser Val Gln Met Glu Lys Pro Val Ile Ala	
145 150 155 160	
gtc agt cta aat tat cgt ctt caa tgc tgg ggt ttt atg tgg agc aag	528
Val Ser Leu Asn Tyr Arg Leu Gln Cys Trp Gly Phe Met Trp Ser Lys	
165 170 175	
gag atg aag gaa gcc gga gta ggg aac ctg gga ctt aga gac caa cga	576
Glu Met Lys Glu Ala Gly Val Gly Asn Leu Gly Leu Arg Asp Gln Arg	
180 185 190	
tta gct ctg cat tgg ata caa gaa aac att gct gcg ttt ggt gga gac	624
Leu Ala Leu His Trp Ile Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp	
195 200 205	
cct gct cag gtt aca att tgg ggt gaa agt gcc gcc gct aat agt gtt	672
Pro Ala Gln Val Thr Ile Trp Gly Glu Ser Ala Gly Ala Asn Ser Val	
210 215 220	
ggc aca cat ctg gtt gct tac gga ggg cgc gat gat ggt ata ttc cgt	720
Gly Thr His Leu Val Ala Tyr Gly Gly Arg Asp Asp Gly Ile Phe Arg	
225 230 235 240	
gca gct atc agt gaa agt ggt gcc cca agt gtt tac caa cgt tat cca	768
Ala Ala Ile Ser Glu Ser Gly Ala Pro Ser Val Tyr Gln Arg Tyr Pro	
245 250 255	
aca cct gct gaa tgg cag ccc tat tat gat ggt att gtg aat gca tca	816
Thr Pro Ala Glu Trp Gln Pro Tyr Tyr Asp Gly Ile Val Asn Ala Ser	
260 265 270	
ggc tgc agt tca gca acg gat act ttg gct tgt ctc cga aca att cca	864
Gly Cys Ser Ser Ala Thr Asp Thr Leu Ala Cys Leu Arg Thr Ile Pro	
275 280 285	
act aac ata ttg cat ggc atc ttt gac aac acg tct att gta ccc atg	912
Thr Asn Ile Leu His Gly Ile Phe Asp Asn Thr Ser Ile Val Pro Met	
290 295 300	
cac gct att tca ggc ctc agc gga gca aaa ttc att cct gtc ata gat	960
His Ala Ile Ser Gly Leu Ser Gly Ala Lys Phe Ile Pro Val Ile Asp	
305 310 315 320	
gac gac ttc att aaa gag agt gcc acg gtt cag ctc cag aag ggc aac	1008
Asp Asp Phe Ile Lys Glu Ser Ala Thr Val Gln Leu Gln Lys Gly Asn	
325 330 335	
ttc gtc aaa gtt ccc tac ttg att gga gct aac gcc gac gaa ggg act	1056
Phe Val Lys Val Pro Tyr Leu Ile Gly Ala Asn Ala Asp Glu Gly Thr	
340 345 350	
gca ttt gct gtg gag gga gtc aac aca gat gct gag ttt cgc gag cta	1104
Ala Phe Ala Val Glu Gly Val Asn Thr Asp Ala Glu Phe Arg Glu Leu	

21078W0.ST25.txt

355	360	365	
gtc aaa ggt tgg ggc ctc aac aac gct acc acg gat atc ttg gag gcc			1152
Val Lys Gly Trp Gly Leu Asn Asn Ala Thr Thr Asp Ile Leu Glu Ala			
370	375	380	
cta tac cca gac att cct cag ata gga atc ccc gcc ata atg gtt gga			1200
Leu Tyr Pro Asp Ile Pro Gln Ile Gly Ile Pro Ala Ile Met Val Gly			
385	390	395	400
agg cca ccg tcc gga tat gga aat caa tac aag cgt gtg gcc gca ttt			1248
Arg Pro Pro Ser Gly Tyr Gly Asn Gln Tyr Lys Arg Val Ala Ala Phe			
405	410	415	
cag ggt gat gtt aac atc cat gcc gca cgt agg ttg acc agt cag atc			1296
Gln Gly Asp Val Asn Ile His Ala Ala Arg Arg Leu Thr Ser Gln Ile			
420	425	430	
tgg tca tcc cgc aat atc tca gta tat agc tac atg ttt gac gtt atc			1344
Trp Ser Ser Arg Asn Ile Ser Val Tyr Ser Tyr Met Phe Asp Val Ile			
435	440	445	
agc cct gga tat ggc ccc tct gct ggt tcc tat gct ggg gct act cat			1392
Ser Pro Gly Tyr Gly Pro Ser Ala Gly Ser Tyr Ala Gly Ala Thr His			
450	455	460	
ggt act gat att ccg tac gtt ttc tat aat ctg gat ggc ctg ggg tat			1440
Gly Thr Asp Ile Pro Tyr Val Phe Tyr Asn Leu Asp Gly Leu Gly Tyr			
465	470	475	480
gac tcg aac aac aag tcc ata gaa agc ata cct aac agt tat tcc cgc			1488
Asp Ser Asn Asn Lys Ser Ile Glu Ser Ile Pro Asn Ser Tyr Ser Arg			
485	490	495	
atg agc aaa att atg tca aga atg tgg gtc agt ttt gtg aca aca ttg			1536
Met Ser Lys Ile Met Ser Arg Met Trp Val Ser Phe Val Thr Thr Leu			
500	505	510	
gac cca aat cat tct gga ggt atg gtc cca cat ccc att cct atg att			1584
Asp Pro Asn His Ser Gly Gly Met Val Pro His Pro Ile Pro Met Ile			
515	520	525	
gcg caa tgt cag acc cga gct gaa tca act atc ttc tta gga act aat			1632
Ala Gln Cys Gln Thr Arg Ala Glu Ser Thr Ile Phe Leu Gly Thr Asn			
530	535	540	
gtt cag tgg ccg cca tac aat atc gat aat ccg gag ata atc ttt ttc			1680
Val Gln Trp Pro Pro Tyr Asn Ile Asp Asn Pro Glu Ile Ile Phe Phe			
545	550	555	560
gat acc gat gtc acg aac ctc aca tat act tgg ccc gca ggt ctt tac			1728
Asp Thr Asp Val Thr Asn Leu Thr Tyr Thr Trp Pro Ala Gly Leu Tyr			
565	570	575	
gcc cac tgg tgg taa			1743
Ala His Trp Trp			
580			

21078WO.ST25.txt

<210> 6

<211> 580

<212> PRT

<213> Aspergillus niger

<400> 6

```

Met Phe Val Ser Ser Leu Ala Leu Leu Ala Leu Ile Ala Pro Leu Ile
1      5      10      15
Ala Ile Ala Val Lys Ile Glu Gln Pro Gly Ile Asn Pro Asn Pro Thr
20      25      30
Ala Thr Val Arg Asn Gly Thr Tyr Tyr Gly Leu His Asn Gln His Tyr
35      40      45
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Gln Pro Ile Gly
50      55      60
Asp Leu Arg Leu Arg Thr Pro Arg Ser Met Asn Thr Ser Trp Pro Val
65      70      75      80
Pro Arg Asn Ala Thr Glu Tyr Ser Pro Ala Cys Val Gly Phe Asn Gln
85      90      95
Thr Glu Gly Ala Ser Glu Ala Cys Leu Thr Leu Asn Val Val Arg Pro
100     105     110
Ala Ser Ile Ala Leu Ser Glu Ser Leu Pro Val Ala Val Trp Ile His
115     120     125
Gly Gly Gly Phe Thr Ser Gly Ser Ser Ser Glu Lys Gln Tyr Asn Leu
130     135     140
Ser Phe Ile Val Asp Gln Ser Val Gln Met Glu Lys Pro Val Ile Ala
145     150     155     160
Val Ser Leu Asn Tyr Arg Leu Gln Cys Trp Gly Phe Met Trp Ser Lys
165     170     175
Glu Met Lys Glu Ala Gly Val Gly Asn Leu Gly Leu Arg Asp Gln Arg
180     185     190
Leu Ala Leu His Trp Ile Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp
195     200     205
Pro Ala Gln Val Thr Ile Trp Gly Glu Ser Ala Gly Ala Asn Ser Val
210     215     220
Gly Thr His Leu Val Ala Tyr Gly Gly Arg Asp Asp Gly Ile Phe Arg
225     230     235     240
Ala Ala Ile Ser Glu Ser Gly Ala Pro Ser Val Tyr Gln Arg Tyr Pro
245     250     255
Thr Pro Ala Glu Trp Gln Pro Tyr Tyr Asp Gly Ile Val Asn Ala Ser
260     265     270
Gly Cys Ser Ser Ala Thr Asp Thr Leu Ala Cys Leu Arg Thr Ile Pro
275     280     285
Thr Asn Ile Leu His Gly Ile Phe Asp Asn Thr Ser Ile Val Pro Met

```

21078WO.ST25.txt

290 295 300
 His Ala Ile Ser Gly Leu Ser Gly Ala Lys Phe Ile Pro Val Ile Asp
 305 310 315 320
 Asp Asp Phe Ile Lys Glu Ser Ala Thr Val Gln Leu Gln Lys Gly Asn
 325 330 335
 Phe Val Lys Val Pro Tyr Leu Ile Gly Ala Asn Ala Asp Glu Gly Thr
 340 345 350
 Ala Phe Ala Val Glu Gly Val Asn Thr Asp Ala Glu Phe Arg Glu Leu
 355 360 365
 Val Lys Gly Trp Gly Leu Asn Asn Ala Thr Thr Asp Ile Leu Glu Ala
 370 375 380
 Leu Tyr Pro Asp Ile Pro Gln Ile Gly Ile Pro Ala Ile Met Val Gly
 385 390 395 400
 Arg Pro Pro Ser Gly Tyr Gly Asn Gln Tyr Lys Arg Val Ala Ala Phe
 405 410 415
 Gln Gly Asp Val Asn Ile His Ala Ala Arg Arg Leu Thr Ser Gln Ile
 420 425 430
 Trp Ser Ser Arg Asn Ile Ser Val Tyr Ser Tyr Met Phe Asp Val Ile
 435 440 445
 Ser Pro Gly Tyr Gly Pro Ser Ala Gly Ser Tyr Ala Gly Ala Thr His
 450 455 460
 Gly Thr Asp Ile Pro Tyr Val Phe Tyr Asn Leu Asp Gly Leu Gly Tyr
 465 470 475 480
 Asp Ser Asn Asn Lys Ser Ile Glu Ser Ile Pro Asn Ser Tyr Ser Arg
 485 490 495
 Met Ser Lys Ile Met Ser Arg Met Trp Val Ser Phe Val Thr Thr Leu
 500 505 510
 Asp Pro Asn His Ser Gly Gly Met Val Pro His Pro Ile Pro Met Ile
 515 520 525
 Ala Gln Cys Gln Thr Arg Ala Glu Ser Thr Ile Phe Leu Gly Thr Asn
 530 535 540
 Val Gln Trp Pro Pro Tyr Asn Ile Asp Asn Pro Glu Ile Ile Phe Phe
 545 550 555 560
 Asp Thr Asp Val Thr Asn Leu Thr Tyr Thr Trp Pro Ala Gly Leu Tyr
 565 570 575
 Ala His Trp Trp
 580

<210> 7

<211> 2769

<212> DNA

<213> Aspergillus niger

21078WO.ST25.txt

<400> 7

gtgaacaatg	attagacttg	gagaacgtgg	tctccgattg	gaagtggact	atctatttaa	60
tagtattgcc	aaggctttct	gatcggcaaa	catattgtcc	tcccgtgggtg	actggtttct	120
cgcctgatgt	gaatagtgat	tatcaattta	tacccttcgt	cagcactgat	tgaataagaa	180
cttacctcac	attgccctca	tttctatgct	ggaaccatgc	acctatTTTT	aagccatccg	240
gccgatctta	ctcacggtat	gggctgactt	tgtatcacaa	cccatacctg	tcgaccgtct	300
aaagtggggg	cagtgacaag	catgatgccg	gtcagcatca	tcagctcaac	aaattctagc	360
caacaacgga	gatcagtggg	ccgacatttg	atgtagaatt	aaacccgcac	acgtcgggaat	420
ggcttcattc	tcggtcttag	tttcccaatc	gaagctgggt	cagcgcccag	acgcggagcg	480
tgggggtggg	accccggtt	ttccccaca	accttggtg	tgggtggcac	tttttcatta	540
gcctccatcc	tgtgcgcaga	tactagagaa	ctctacatca	tgccatcgag	gtttgttagt	600
tagatttggt	aactagctga	gcggtgtagg	tgcattgccg	acggtgagtt	tgtctatctt	660
ttgtatagcc	ggaagccgaa	ggtacccgcg	gtcatggcta	tataaggctt	gtatatccca	720
tgtctgggta	gatgggacaa	caagaacggc	gatccgatag	aatcatgggtg	cagggtgtgg	780
cttttggaact	gctcgggctg	gctgcctctg	ctttgggcac	ttatgcgcc	tactacgcga	840
atgtgacatg	ggagcaacca	cggactctgt	ccaactgggtc	caaccttacc	gtcgagacac	900
ggacagggac	gttcattggg	atgctcaatg	acacttaccc	agacgttcga	cagtttctgc	960
gagttcctta	tgccaaggta	attctctcgc	tgtacacatg	tcatactgtg	tctgacatga	1020
ccagcctcct	attgggggatt	taagatggct	tcctcctcat	cggcttgaca	actcaagcag	1080
aacatatgac	tccaccttct	atggcccagg	taagtagtct	tccatacaac	tatgagcagt	1140
tccaattaac	ccgagttcag	cctgtccgca	gtatgttcca	gcagagagcg	atTTTTggaa	1200
tgaatatgaa	ccggagaatt	tgctgctcaa	tgctcggcgaa	aggctcaacc	agggtctctac	1260
ggcatgggtcc	tcgtcagagg	attgcctgtc	cctagcggta	tggactccat	cgtatgctaa	1320
tgagacatcc	aagctgccag	ttgcgtgtt	tgtcacggga	ggtgggtggca	tcacaggggg	1380
tatcaacatt	ccgtcccagc	tgccctctgc	ttgggtatct	cgctctcagg	agcatatcgt	1440
tgttaccatc	aattaccgcg	tcaatatatt	tggcagtaag	tatttgctct	atatttgcaa	1500
atattagcct	gacatgtata	gatcccaaat	cgcgtgcgtt	gaatgatacg	tcgcttacgc	1560
tgatggacgt	gcgcgtgct	gtggagtggg	tatatgagaa	cattgaagcg	ttcgggtggta	1620
atccccgaaa	tattatgggtc	agactacaag	tttctctca	catgactaga	gctaacagta	1680
agcagctatg	gggacagtca	caaggtgctt	tgtgacgca	tctgtacacc	ctcgcatggc	1740
cagaagagcc	tcttgccgcc	aagttcggcg	tcatctccca	aggagcatct	gccacactca	1800
acctctctac	cacgcccgat	gtgtaccaag	actttgacat	cgtggccaag	ggactaggct	1860
gcaattatgg	tgatgatgcc	gaggccgagc	tggagtgcac	gcgtgggatt	tcctgggtgc	1920
agatcgagga	gtatatcaac	cgctacaata	gctctccttc	tattgctttc	acgaactata	1980
ttcgtatgta	cccatcttgc	tcttttaact	gcccctacta	acaatatcag	ccgatgagaa	2040
atacatcttc	tccgacgaaa	gacagcgtaa	ccttgagcgg	aaggttgccc	gaggcccgtc	2100
aattcgatct	gacacggcgc	gagaattccc	tagcacaaac	acgacctcag	taaatattga	2160
agaaggcgaa	tcagactgtc	tggcagtgtc	tgaccttgcg	ctacgtgcgt	ccattgggct	2220
cgagacctat	cgctactact	gggctgggtat	gtccaatgac	ttccatact	gaagatagtg	2280
ctaacataaa	caggcaactt	ctccaatatc	agtcccgtac	cgtggctagg	agcattccac	2340
tggaccgacc	tgctgatgat	cttcggtacg	tataatctgg	acgtcggcga	gatctcgag	2400
ttggaagtcg	acacctctgc	cacgatgcaa	gattatctac	tcgcctttct	gaaggactca	2460
tcaaccgtca	gcgagacggt	cggatggccg	ttatatctgg	gcaacgagac	caacggagga	2520
ctcatcctgg	agttcggtaa	cggcacagca	gtgcggacca	tcacaggtga	ctggctcgac	2580

21078WO.ST25.txt

gcgggatgtt tcaattcatc tatcccatc agaattctggg ggtagcctat acacaccatc	2640
atcagagtag tatatacatc atatccacaa atccatctcc acctatatac ataaacccca	2700
actgaatcta caacagcgcc tggtccttct tcccctcccc ctctttaatt tccctcgcct	2760
tctcccat	2769

<210> 8

<211> 1623

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1623)

<400> 8

atg gtg cag ggt gtg gct ttt gga ctg ctc ggg ctg gct gcc tct gct	48
Met Val Gln Gly Val Ala Phe Gly Leu Leu Gly Leu Ala Ala Ser Ala	
1 5 10 15	
ttg ggc act tat gcg ccc tac tac gcg aat ttg aca tgg gag caa cca	96
Leu Gly Thr Tyr Ala Pro Tyr Tyr Ala Asn Leu Thr Trp Glu Gln Pro	
20 25 30	
cgg act ctg tcc aac tgg tcc aac ctt acc gtc gag aca cgg aca ggg	144
Arg Thr Leu Ser Asn Trp Ser Asn Leu Thr Val Glu Thr Arg Thr Gly	
35 40 45	
acg ttc att ggt atg ctc aat gac act tac cca gac gtt cga cag ttt	192
Thr Phe Ile Gly Met Leu Asn Asp Thr Tyr Pro Asp Val Arg Gln Phe	
50 55 60	
ctg cga gtt cct tat gcc aag cct cct att ggg gat tta aga tgg ctt	240
Leu Arg Val Pro Tyr Ala Lys Pro Pro Ile Gly Asp Leu Arg Trp Leu	
65 70 75 80	
cct cct cat cgg ctt gac aac tca agc aga aca tat gac tcc acc ttc	288
Pro Pro His Arg Leu Asp Asn Ser Ser Arg Thr Tyr Asp Ser Thr Phe	
85 90 95	
tat ggc cca gcc tgt ccg cag tat gtt cca gca gag agc gat ttt tgg	336
Tyr Gly Pro Ala Cys Pro Gln Tyr Val Pro Ala Glu Ser Asp Phe Trp	
100 105 110	
aat gaa tat gaa ccg gag aat ttg ctg ctc aat gtc ggc gaa agg ctc	384
Asn Glu Tyr Glu Pro Glu Asn Leu Leu Leu Asn Val Gly Glu Arg Leu	
115 120 125	
aac cag ggc tct acg gca tgg tcc tcg tca gag gat tgc ctg tcc cta	432
Asn Gln Gly Ser Thr Ala Trp Ser Ser Ser Glu Asp Cys Leu Ser Leu	
130 135 140	
gcg gta tgg act cca tcg tat gct aat gag aca tcc aag ctg cca gtt	480

21078W0.ST25.txt

Ala Val Trp Thr Pro Ser Tyr Ala Asn Glu Thr Ser Lys Leu Pro Val	
145 150 155 160	
gcg ctg ttt gtc acg gga ggt ggt ggc atc aca ggg ggt atc aac att	528
Ala Leu Phe Val Thr Gly Gly Gly Gly Ile Thr Gly Gly Ile Asn Ile	
165 170 175	
ccg tcc cag ctg ccc tct gct tgg gta tct cgc tct cag gag cat atc	576
Pro Ser Gln Leu Pro Ser Ala Trp Val Ser Arg Ser Gln Glu His Ile	
180 185 190	
gtt gtt acc atc aat tac cgc gtc aat att ttt ggc aat ccc aaa tcg	624
Val Val Thr Ile Asn Tyr Arg Val Asn Ile Phe Gly Asn Pro Lys Ser	
195 200 205	
cgt gcg ttg aat gat acg tcg ctt acg ctg atg gac gtg cgc gct gct	672
Arg Ala Leu Asn Asp Thr Ser Leu Thr Leu Met Asp Val Arg Ala Ala	
210 215 220	
gtg gag tgg gta tat gag aac att gaa gcg ttc ggt ggt aat ccc gaa	720
Val Glu Trp Val Tyr Glu Asn Ile Glu Ala Phe Gly Gly Asn Pro Glu	
225 230 235 240	
aat att atg gtc aga cta caa gtt tcc tct cac atg act aga gct aac	768
Asn Ile Met Val Arg Leu Gln Val Ser Ser His Met Thr Arg Ala Asn	
245 250 255	
agt aag cag cta tgg gga cag tca caa ggt gct ttg ctg acg cat ctg	816
Ser Lys Gln Leu Trp Gly Gln Ser Gln Gly Ala Leu Leu Thr His Leu	
260 265 270	
tac acc ctc gca tgg cca gaa gag cct ctt gcc gcc aag ttc ggc gtc	864
Tyr Thr Leu Ala Trp Pro Glu Glu Pro Leu Ala Ala Lys Phe Gly Val	
275 280 285	
atc tcc caa gga gca tct gcc aca ctc aac ctc tct acc acg ccc gat	912
Ile Ser Gln Gly Ala Ser Ala Thr Leu Asn Leu Ser Thr Thr Pro Asp	
290 295 300	
gtg tac caa gac ttt gac atc gtg gcc aag gga cta ggc tgc aat tat	960
Val Tyr Gln Asp Phe Asp Ile Val Ala Lys Gly Leu Gly Cys Asn Tyr	
305 310 315 320	
ggg gat gat gcc gag gcc gag ctg gag tgc atg cgt ggg att tcc tgg	1008
Gly Asp Asp Ala Glu Ala Glu Leu Glu Cys Met Arg Gly Ile Ser Trp	
325 330 335	
gtg cag atc gag gag tat atc aac cgc tac aat agc tct cct tct att	1056
Val Gln Ile Glu Glu Tyr Ile Asn Arg Tyr Asn Ser Ser Pro Ser Ile	
340 345 350	
gct ttc acg aac tat att ccc gat gag aaa tac atc ttc tcc gac gaa	1104
Ala Phe Thr Asn Tyr Ile Pro Asp Glu Lys Tyr Ile Phe Ser Asp Glu	
355 360 365	
aga cag cgt tac ctt gag cgg aag gtt gcc cga ggc ccg tca att cga	1152
Arg Gln Arg Tyr Leu Glu Arg Lys Val Ala Arg Gly Pro Ser Ile Arg	
370 375 380	

21078W0.ST25.txt

```

tct gac acg gcg cga gaa ttc cct agc aca aac acg acc tca gta aat      1200
Ser Asp Thr Ala Arg Glu Phe Pro Ser Thr Asn Thr Thr Ser Val Asn
385              390              395              400
att gaa gaa ggc gaa tca gac tgt ctg gca gtg act gac ctt gcg cta      1248
Ile Glu Glu Gly Glu Ser Asp Cys Leu Ala Val Thr Asp Leu Ala Leu
405              410              415
cgt gcg tcc att ggg ctc gag acc tat cgc tac tac tgg gct ggc aac      1296
Arg Ala Ser Ile Gly Leu Glu Thr Tyr Arg Tyr Tyr Trp Ala Gly Asn
420              425              430
ttc tcc aat atc agt ccc gta ccg tgg cta gga gca ttc cac tgg acc      1344
Phe Ser Asn Ile Ser Pro Val Pro Trp Leu Gly Ala Phe His Trp Thr
435              440              445
gac ctg ctg atg atc ttc ggt acg tat aat ctg gac gtc ggc gag atc      1392
Asp Leu Leu Met Ile Phe Gly Thr Tyr Asn Leu Asp Val Gly Glu Ile
450              455              460
tcg cag ttg gaa gtc gac acc tct gcc acg atg caa gat tat cta ctc      1440
Ser Gln Leu Glu Val Asp Thr Ser Ala Thr Met Gln Asp Tyr Leu Leu
465              470              475              480
gcc ttt ctg aag gac tca tca acc gtc agc gag acg gtc gga tgg ccg      1488
Ala Phe Leu Lys Asp Ser Ser Thr Val Ser Glu Thr Val Gly Trp Pro
485              490              495
tta tat ctg ggc aac gag acc aac gga gga ctc atc ctg gag ttc ggt      1536
Leu Tyr Leu Gly Asn Glu Thr Asn Gly Gly Leu Ile Leu Glu Phe Gly
500              505              510
aac ggc aca gca gtg cgg acc atc aca ggt gac tgg ctc gac gcg gga      1584
Asn Gly Thr Ala Val Arg Thr Ile Thr Gly Asp Trp Leu Asp Ala Gly
515              520              525
tgt ttc aat tca tct atc cca ttc aga atc tgg ggg tag      1623
Cys Phe Asn Ser Ser Ile Pro Phe Arg Ile Trp Gly
530              535              540

```

<210> 9

<211> 540

<212> PRT

<213> *Aspergillus niger*

<400> 9

```

Met Val Gln Gly Val Ala Phe Gly Leu Leu Gly Leu Ala Ala Ser Ala
1              5              10              15
Leu Gly Thr Tyr Ala Pro Tyr Tyr Ala Asn Leu Thr Trp Glu Gln Pro
20              25              30
Arg Thr Leu Ser Asn Trp Ser Asn Leu Thr Val Glu Thr Arg Thr Gly
35              40              45

```

21078W0.ST25.txt

Thr Phe Ile Gly Met Leu Asn Asp Thr Tyr Pro Asp Val Arg Gln Phe
 50 55 60
 Leu Arg Val Pro Tyr Ala Lys Pro Pro Ile Gly Asp Leu Arg Trp Leu
 65 70 75 80
 Pro Pro His Arg Leu Asp Asn Ser Ser Arg Thr Tyr Asp Ser Thr Phe
 85 90 95
 Tyr Gly Pro Ala Cys Pro Gln Tyr Val Pro Ala Glu Ser Asp Phe Trp
 100 105 110
 Asn Glu Tyr Glu Pro Glu Asn Leu Leu Leu Asn Val Gly Glu Arg Leu
 115 120 125
 Asn Gln Gly Ser Thr Ala Trp Ser Ser Ser Glu Asp Cys Leu Ser Leu
 130 135 140
 Ala Val Trp Thr Pro Ser Tyr Ala Asn Glu Thr Ser Lys Leu Pro Val
 145 150 155 160
 Ala Leu Phe Val Thr Gly Gly Gly Gly Ile Thr Gly Gly Ile Asn Ile
 165 170 175
 Pro Ser Gln Leu Pro Ser Ala Trp Val Ser Arg Ser Gln Glu His Ile
 180 185 190
 Val Val Thr Ile Asn Tyr Arg Val Asn Ile Phe Gly Asn Pro Lys Ser
 195 200 205
 Arg Ala Leu Asn Asp Thr Ser Leu Thr Leu Met Asp Val Arg Ala Ala
 210 215 220
 Val Glu Trp Val Tyr Glu Asn Ile Glu Ala Phe Gly Gly Asn Pro Glu
 225 230 235 240
 Asn Ile Met Val Arg Leu Gln Val Ser Ser His Met Thr Arg Ala Asn
 245 250 255
 Ser Lys Gln Leu Trp Gly Gln Ser Gln Gly Ala Leu Leu Thr His Leu
 260 265 270
 Tyr Thr Leu Ala Trp Pro Glu Glu Pro Leu Ala Ala Lys Phe Gly Val
 275 280 285
 Ile Ser Gln Gly Ala Ser Ala Thr Leu Asn Leu Ser Thr Thr Pro Asp
 290 295 300
 Val Tyr Gln Asp Phe Asp Ile Val Ala Lys Gly Leu Gly Cys Asn Tyr
 305 310 315 320
 Gly Asp Asp Ala Glu Ala Glu Leu Glu Cys Met Arg Gly Ile Ser Trp
 325 330 335
 Val Gln Ile Glu Glu Tyr Ile Asn Arg Tyr Asn Ser Ser Pro Ser Ile
 340 345 350
 Ala Phe Thr Asn Tyr Ile Pro Asp Glu Lys Tyr Ile Phe Ser Asp Glu
 355 360 365
 Arg Gln Arg Tyr Leu Glu Arg Lys Val Ala Arg Gly Pro Ser Ile Arg
 370 375 380
 Ser Asp Thr Ala Arg Glu Phe Pro Ser Thr Asn Thr Thr Ser Val Asn
 385 390 395 400

21078WO.ST25.txt

Ile Glu Glu Gly Glu Ser Asp Cys Leu Ala Val Thr Asp Leu Ala Leu
 405 410 415
 Arg Ala Ser Ile Gly Leu Glu Thr Tyr Arg Tyr Tyr Trp Ala Gly Asn
 420 425 430
 Phe Ser Asn Ile Ser Pro Val Pro Trp Leu Gly Ala Phe His Trp Thr
 435 440 445
 Asp Leu Leu Met Ile Phe Gly Thr Tyr Asn Leu Asp Val Gly Glu Ile
 450 455 460
 Ser Gln Leu Glu Val Asp Thr Ser Ala Thr Met Gln Asp Tyr Leu Leu
 465 470 475 480
 Ala Phe Leu Lys Asp Ser Ser Thr Val Ser Glu Thr Val Gly Trp Pro
 485 490 495
 Leu Tyr Leu Gly Asn Glu Thr Asn Gly Gly Leu Ile Leu Glu Phe Gly
 500 505 510
 Asn Gly Thr Ala Val Arg Thr Ile Thr Gly Asp Trp Leu Asp Ala Gly
 515 520 525
 Cys Phe Asn Ser Ser Ile Pro Phe Arg Ile Trp Gly
 530 535 540

<210> 10

<211> 3235

<212> DNA

<213> *Aspergillus niger*

<400> 10

gttttcaatt	tggactgaat	tttggcggca	tttcttgtat	aaaattaaaa	ggggcgttga	60
ctggattttg	gtacttggga	tttattctta	gctttgactg	tacatagttt	gggcgtgggt	120
tgatagccga	cgatcggccg	acccacgaac	cagatttgca	tatgattaca	ttccttcaat	180
tttgggccga	gtcccaacct	gcctttcaac	cccaacaact	acaagcacgt	tgtgtttgct	240
acattgactc	actcgatatt	gctgaaccat	gcaggccgcc	caactgagtt	attacaccaa	300
gcatgcgaat	cggaaagtgc	gacaaagcgg	gtgaaatgtc	cgagttggcg	aaccaaagcg	360
caacggtcga	ggctcctttc	cccgcagagg	cagccattct	gcagcctttg	aactgcgggg	420
gaaacggcat	ttgatcaact	cggcactgat	gcagtgaacca	acaggatgtt	agcaatgttg	480
gcctaataata	ttcttactga	tctgctgata	cgtccctccc	ttgcatcagc	ctcggtttgc	540
gcatgagaac	gggttcgaac	gttcctgggc	caccgggttg	gcgtgatatt	ctccgcccac	600
gctgtctgtc	cccctgatgg	gaaaccttcg	gatcagcgat	catcaggcca	gttggctatg	660
agaatagggg	ctttgctgtc	ttgatgccta	aaatgcaggt	ctcatagcaa	gatccacagc	720
cgaggaggca	catggcgatg	tcgaaaccca	tgggagctga	tttttcgggt	ctcggatcgt	780
gctccaagac	atagaaggat	attgagcact	tgaacgaag	gggtgaaaaa	tggaaactgta	840
tatagagtta	ctcccagccc	gatccgagag	cctatgacct	atagcggtac	agatcatggc	900
catcatgaag	gccctccttt	ggctctccct	ttccctcgcc	gtctgggcga	ctccagttca	960
acgggatgca	gctcctactg	tcactattgc	gcatccatcg	gccaccgtca	ttggaaaatc	1020
tggcaatgtc	gagagcttca	acaatatattcc	ctttgcgcag	gccccacag	gctcgtgcg	1080

21078WO.ST25.txt

tctgaagccc	ccacaaccct	tggaaactgc	cctcggcact	gttcaggcca	caggagcctc	1140
gcaatcgtgt	ccgcagatgt	acttcaccac	ggatgagagc	gaattcccga	catcgggtcat	1200
tggcctcctc	gctgatctcc	ctttggtaca	gtcggctacc	aatgctctcg	aggattgcct	1260
gaacattgac	attcggcgtc	cggccgggac	caccgcggac	tcgaagctgc	ctgtgctggt	1320
ctggatcttt	ggcggaggct	ttgaacttgg	ttcaaaggcg	atgtatgatg	gtacaacgat	1380
ggtatcatcg	tcgatagaca	agaacatgcc	tatcgtgttt	gtagcaatga	attatcgcgt	1440
gggagggttc	gggttcttgc	ccggaaagga	gacccctggag	gacgggtccg	cgaacctagg	1500
gctcctggac	caacgccttg	ccctgcagtg	ggttgccgac	aacatcgagg	cctttggtgg	1560
agaccggac	aaggtgacga	tttggggaga	atcagcagga	gccatttccg	tttttgatca	1620
gatgatcttg	tacgacggaa	acatcactta	caaggataag	cccttgttcc	ggggggccat	1680
catggactcc	ggtagtgttg	ttcccgcaga	ccccgtcgat	ggggtcaagg	gacagcaagt	1740
atatgatgcg	gtagtggaat	ctgcaggctg	ttcctcttct	aacgacaccc	tagcttgtct	1800
gcgtgaacta	gactacaccg	acttcctcaa	tgcggcaaac	tccgtgccag	gcattttaag	1860
ctaccattct	gtggcgttat	catatgtgcc	tcgaccggac	gggacggcgt	tgtcggcatc	1920
accggacgtt	ttgggcaaag	cagggaaata	tgctcgggtc	ccgttcatcg	tgggcgacca	1980
agaggatgag	gggaccttat	tcgccttggt	tcagtccaac	attacgacga	tcgacgaggt	2040
ggtcgactac	ctggcctcat	acttcttcta	tgacgctagc	cgagagcagc	ttgaagaact	2100
agtggccctg	taccagaca	ccaccacgta	cgggtctccg	ttcaggacag	gcgcggccaa	2160
caactggtat	ccgcaattta	agcgattggc	cgccattctc	ggcgacttgg	tcttcaccat	2220
taccggcg	gcattcctct	cgtatgcaga	ggaaatctcc	cctgatcttc	cgaactggtc	2280
gtacctggcg	acctatgact	atggcacccc	agttctgggg	accttccacg	gaagtgacct	2340
gctgcagggtg	ttctatggga	tcaagccaaa	ctatgcagct	agttctagcc	acacgtacta	2400
tctgagcttt	gtgtatacgc	tggatccgaa	ctccaaccgg	ggggagtaca	ttgagtggcc	2460
gcagtggaag	gaatcgcggc	agttgatgaa	tttcggagcg	aacgacgcca	gtctccttac	2520
ggatgatttc	cgcaacggga	catatgagtt	catcctgcag	aataccgcgg	cgttccacat	2580
ctgatgccat	tggcggaggg	gtccggacgg	tcaggaactt	agccttatga	gatgaatgat	2640
ggacgtgtct	ggcctcgaa	aaggatatat	ggggatcatg	atagtactag	ccatattaat	2700
gaagggcata	taccacgcgt	tggacctgcg	ttatagcttc	ccgttagtta	tagtaccatc	2760
gttataccag	ccaatcaagt	caccacgcac	gaccggggac	ggcgaatccc	cgggaattga	2820
aagaaattgc	atcccaggcc	agtgaggcca	gcgattggcc	acctctccaa	ggcacagggc	2880
cattctgcag	cgctgggtga	ttcatcgcaa	tttcccccg	cccggcccga	caccgctata	2940
ggctggttct	cccacaccat	cggagattcg	tcgcctaattg	tctcgtccgt	tcacaagctg	3000
aagagcttga	agtggcgaga	tgtctctgca	ggaattcaag	ctagatgcta	agcgatattg	3060
catggcaata	tgtgttgatg	catgtgcttc	ttccttcagc	ttcccctcgt	gcagatgagg	3120
tttggctata	aattgaagtg	gttggtcggg	gttccgtgag	gggctgaagt	gcttcctccc	3180
ttttagacgc	aactgagagc	ctgagcttca	tccccagcat	cattacacct	cagca	3235

<210> 11

<211> 1689

<212> DNA

<213> *Aspergillus niger*

<220>

21078WO.ST25.txt

<221> CDS

<222> (1)..(1689)

<400> 11

atg gcc atc atg aag gcc ctc ctt tgg ctc tcc ctt tcc ctc gcc gtc	48
Met Ala Ile Met Lys Ala Leu Leu Trp Leu Ser Leu Ser Leu Ala Val	
1 5 10 15	
tgg gcg act cca gtt caa cgg gat gca gct cct act gtc act att gcg	96
Trp Ala Thr Pro Val Gln Arg Asp Ala Ala Pro Thr Val Thr Ile Ala	
20 25 30	
cat cca tcg gcc acc gtc att gga aaa tct ggc aat gtc gag agc ttc	144
His Pro Ser Ala Thr Val Ile Gly Lys Ser Gly Asn Val Glu Ser Phe	
35 40 45	
aac aat att ccc ttt gcg cag gcc ccc aca ggc tcg ctg cgt ctg aag	192
Asn Asn Ile Pro Phe Ala Gln Ala Pro Thr Gly Ser Leu Arg Leu Lys	
50 55 60	
ccc cca caa ccc ttg gaa act gcc ctc ggc act gtt cag gcc aca gga	240
Pro Pro Gln Pro Leu Glu Thr Ala Leu Gly Thr Val Gln Ala Thr Gly	
65 70 75 80	
gcc tcg caa tcg tgt ccg cag atg tac ttc acc acg gat gag agc gaa	288
Ala Ser Gln Ser Cys Pro Gln Met Tyr Phe Thr Thr Asp Glu Ser Glu	
85 90 95	
ttc ccg aca tcg gtc att ggc ctc ctc gct gat ctc cct ttg gta cag	336
Phe Pro Thr Ser Val Ile Gly Leu Leu Ala Asp Leu Pro Leu Val Gln	
100 105 110	
tcg gct acc aat gct ctc gag gat tgc ctg aac att gac att cgg cgt	384
Ser Ala Thr Asn Ala Leu Glu Asp Cys Leu Asn Ile Asp Ile Arg Arg	
115 120 125	
ccg gcc ggg acc acc gcg gac tcg aag ctg cct gtg ctg gtc tgg atc	432
Pro Ala Gly Thr Thr Ala Asp Ser Lys Leu Pro Val Leu Val Trp Ile	
130 135 140	
ttt ggc gga ggc ttt gaa ctt ggt tca aag gcg atg tat gat ggt aca	480
Phe Gly Gly Gly Phe Glu Leu Gly Ser Lys Ala Met Tyr Asp Gly Thr	
145 150 155 160	
acg atg gta tca tcg tcg ata gac aag aac atg cct atc gtg ttt gta	528
Thr Met Val Ser Ser Ser Ile Asp Lys Asn Met Pro Ile Val Phe Val	
165 170 175	
gca atg aat tat cgc gtg gga ggt ttc ggg ttc ttg ccc gga aag gag	576
Ala Met Asn Tyr Arg Val Gly Gly Phe Gly Phe Leu Pro Gly Lys Glu	
180 185 190	
atc ctg gag gac ggg tcc gcg aac cta ggg ctc ctg gac caa cgc ctt	624
Ile Leu Glu Asp Gly Ser Ala Asn Leu Gly Leu Leu Asp Gln Arg Leu	
195 200 205	
gcc ctg cag tgg gtt gcc gac aac atc gag gcc ttt ggt gga gac ccg	672

21078W0.ST25.txt

Ala Leu Gln Trp Val	Ala Asp Asn Ile Glu Ala Phe Gly Gly Asp Pro	
210	215	220
gac aag gtg acg att tgg gga gaa tca gca gga gcc att tcc gtt ttt		720
Asp Lys Val Thr Ile Trp Gly Glu Ser Ala Gly Ala Ile Ser Val Phe		
225	230	235
gat cag atg atc ttg tac gac gga aac atc act tac aag gat aag ccc		768
Asp Gln Met Ile Leu Tyr Asp Gly Asn Ile Thr Tyr Lys Asp Lys Pro		
245	250	255
ttg ttc cgg ggg gcc atc atg gac tcc ggt agt gtt gtt ccc gca gac		816
Leu Phe Arg Gly Ala Ile Met Asp Ser Gly Ser Val Val Pro Ala Asp		
260	265	270
ccc gtc gat ggg gtc aag gga cag caa gta tat gat gcg gta gtg gaa		864
Pro Val Asp Gly Val Lys Gly Gln Gln Val Tyr Asp Ala Val Val Glu		
275	280	285
tct gca ggc tgt tcc tct tct aac gac acc cta gct tgt ctg cgt gaa		912
Ser Ala Gly Cys Ser Ser Ser Asn Asp Thr Leu Ala Cys Leu Arg Glu		
290	295	300
cta gac tac acc gac ttc ctc aat gcg gca aac tcc gtg cca ggc att		960
Leu Asp Tyr Thr Asp Phe Leu Asn Ala Ala Asn Ser Val Pro Gly Ile		
305	310	315
tta agc tac cat tct gtg gcg tta tca tat gtg cct cga ccg gac ggg		1008
Leu Ser Tyr His Ser Val Ala Leu Ser Tyr Val Pro Arg Pro Asp Gly		
325	330	335
acg gcg ttg tcg gca tca ccg gac gtt ttg ggc aaa gca ggg aaa tat		1056
Thr Ala Leu Ser Ala Ser Pro Asp Val Leu Gly Lys Ala Gly Lys Tyr		
340	345	350
gct cgg gtc ccg ttc atc gtg ggc gac caa gag gat gag ggg acc tta		1104
Ala Arg Val Pro Phe Ile Val Gly Asp Gln Glu Asp Glu Gly Thr Leu		
355	360	365
ttc gcc ttg ttt cag tcc aac att acg acg atc gac gag gtg gtc gac		1152
Phe Ala Leu Phe Gln Ser Asn Ile Thr Thr Ile Asp Glu Val Val Asp		
370	375	380
tac ctg gcc tca tac ttc ttc tat gac gct agc cga gag cag ctt gaa		1200
Tyr Leu Ala Ser Tyr Phe Phe Tyr Asp Ala Ser Arg Glu Gln Leu Glu		
385	390	395
gaa cta gtg gcc ctg tac cca gac acc acc acg tac ggg tct ccg ttc		1248
Glu Leu Val Ala Leu Tyr Pro Asp Thr Thr Thr Tyr Gly Ser Pro Phe		
405	410	415
agg aca ggc gcg gcc aac aac tgg tat ccg caa ttt aag cga ttg gcc		1296
Arg Thr Gly Ala Ala Asn Asn Trp Tyr Pro Gln Phe Lys Arg Leu Ala		
420	425	430
gcc att ctc ggc gac ttg gtc ttc acc att acc cgg cgg gca ttc ctc		1344
Ala Ile Leu Gly Asp Leu Val Phe Thr Ile Thr Arg Arg Ala Phe Leu		
435	440	445

21078W0.ST25.txt

tcg tat gca gag gaa atc tcc cct gat ctt ccg aac tgg tcg tac ctg	1392
Ser Tyr Ala Glu Glu Ile Ser Pro Asp Leu Pro Asn Trp Ser Tyr Leu	
450 455 460	
gcg acc tat gac tat ggc acc cca gtt ctg ggg acc ttc cac gga agt	1440
Ala Thr Tyr Asp Tyr Gly Thr Pro Val Leu Gly Thr Phe His Gly Ser	
465 470 475 480	
gac ctg ctg cag gtg ttc tat ggg atc aag cca aac tat gca gct agt	1488
Asp Leu Leu Gln Val Phe Tyr Gly Ile Lys Pro Asn Tyr Ala Ala Ser	
485 490 495	
tct agc cac acg tac tat ctg agc ttt gtg tat acg ctg gat ccg aac	1536
Ser Ser His Thr Tyr Tyr Leu Ser Phe Val Tyr Thr Leu Asp Pro Asn	
500 505 510	
tcc aac cgg ggg gag tac att gag tgg ccg cag tgg aag gaa tcg cgg	1584
Ser Asn Arg Gly Glu Tyr Ile Glu Trp Pro Gln Trp Lys Glu Ser Arg	
515 520 525	
cag ttg atg aat ttc gga gcg aac gac gcc agt ctc ctt acg gat gat	1632
Gln Leu Met Asn Phe Gly Ala Asn Asp Ala Ser Leu Leu Thr Asp Asp	
530 535 540	
ttc cgc aac ggg aca tat gag ttc atc ctg cag aat acc gcg gcg ttc	1680
Phe Arg Asn Gly Thr Tyr Glu Phe Ile Leu Gln Asn Thr Ala Ala Phe	
545 550 555 560	
cac atc tga	1689
His Ile	

<210> 12

<211> 562

<212> PRT

<213> Aspergillus niger

<400> 12

Met Ala Ile Met Lys Ala Leu Leu Trp Leu Ser Leu Ser Leu Ala Val	
1 5 10 15	
Trp Ala Thr Pro Val Gln Arg Asp Ala Ala Pro Thr Val Thr Ile Ala	
20 25 30	
His Pro Ser Ala Thr Val Ile Gly Lys Ser Gly Asn Val Glu Ser Phe	
35 40 45	
Asn Asn Ile Pro Phe Ala Gln Ala Pro Thr Gly Ser Leu Arg Leu Lys	
50 55 60	
Pro Pro Gln Pro Leu Glu Thr Ala Leu Gly Thr Val Gln Ala Thr Gly	
65 70 75 80	
Ala Ser Gln Ser Cys Pro Gln Met Tyr Phe Thr Thr Asp Glu Ser Glu	
85 90 95	
Phe Pro Thr Ser Val Ile Gly Leu Leu Ala Asp Leu Pro Leu Val Gln	

21078WO.ST25.txt

	100		105		110
Ser Ala Thr	Asn Ala Leu Glu Asp Cys Leu Asn Ile	Asp Ile Arg Arg			
	115		120		125
Pro Ala Gly Thr Thr	Ala Asp Ser Lys Leu Pro Val	Leu Val Trp Ile			
	130		135		140
Phe Gly Gly Gly Phe	Glu Leu Gly Ser Lys Ala Met Tyr Asp Gly Thr				
145		150		155	160
Thr Met Val Ser Ser	Ser Ile Asp Lys Asn Met Pro Ile Val Phe Val				
	165		170		175
Ala Met Asn Tyr Arg	Val Gly Gly Phe Gly Phe Leu Pro Gly Lys Glu				
	180		185		190
Ile Leu Glu Asp Gly	Ser Ala Asn Leu Gly Leu Leu Asp Gln Arg Leu				
	195		200		205
Ala Leu Gln Trp Val	Ala Asp Asn Ile Glu Ala Phe Gly Gly Asp Pro				
	210		215		220
Asp Lys Val Thr Ile	Trp Gly Glu Ser Ala Gly Ala Ile Ser Val Phe				
225		230		235	240
Asp Gln Met Ile Leu	Tyr Asp Gly Asn Ile Thr Tyr Lys Asp Lys Pro				
	245		250		255
Leu Phe Arg Gly Ala	Ile Met Asp Ser Gly Ser Val Val Pro Ala Asp				
	260		265		270
Pro Val Asp Gly Val	Lys Gly Gln Gln Val Tyr Asp Ala Val Val Glu				
	275		280		285
Ser Ala Gly Cys Ser	Ser Ser Asn Asp Thr Leu Ala Cys Leu Arg Glu				
	290		295		300
Leu Asp Tyr Thr Asp	Phe Leu Asn Ala Ala Asn Ser Val Pro Gly Ile				
305		310		315	320
Leu Ser Tyr His Ser	Val Ala Leu Ser Tyr Val Pro Arg Pro Asp Gly				
	325		330		335
Thr Ala Leu Ser Ala	Ser Pro Asp Val Leu Gly Lys Ala Gly Lys Tyr				
	340		345		350
Ala Arg Val Pro Phe	Ile Val Gly Asp Gln Glu Asp Glu Gly Thr Leu				
	355		360		365
Phe Ala Leu Phe Gln	Ser Asn Ile Thr Thr Ile Asp Glu Val Val Asp				
	370		375		380
Tyr Leu Ala Ser Tyr	Phe Phe Tyr Asp Ala Ser Arg Glu Gln Leu Glu				
385		390		395	400
Glu Leu Val Ala Leu	Tyr Pro Asp Thr Thr Thr Tyr Gly Ser Pro Phe				
	405		410		415
Arg Thr Gly Ala Ala	Asn Asn Trp Tyr Pro Gln Phe Lys Arg Leu Ala				
	420		425		430
Ala Ile Leu Gly Asp	Leu Val Phe Thr Ile Thr Arg Arg Ala Phe Leu				
	435		440		445
Ser Tyr Ala Glu Glu	Ile Ser Pro Asp Leu Pro Asn Trp Ser Tyr Leu				

21078WO.ST25.txt

450 455 460
 Ala Thr Tyr Asp Tyr Gly Thr Pro Val Leu Gly Thr Phe His Gly Ser
 465 470 475 480
 Asp Leu Leu Gln Val Phe Tyr Gly Ile Lys Pro Asn Tyr Ala Ala Ser
 485 490 495
 Ser Ser His Thr Tyr Tyr Leu Ser Phe Val Tyr Thr Leu Asp Pro Asn
 500 505 510
 Ser Asn Arg Gly Glu Tyr Ile Glu Trp Pro Gln Trp Lys Glu Ser Arg
 515 520 525
 Gln Leu Met Asn Phe Gly Ala Asn Asp Ala Ser Leu Leu Thr Asp Asp
 530 535 540
 Phe Arg Asn Gly Thr Tyr Glu Phe Ile Leu Gln Asn Thr Ala Ala Phe
 545 550 555 560
 His Ile

<210> 13

<211> 2097

<212> DNA

<213> *Aspergillus niger*

<400> 13

cctggctgac	gctataccga	agacgatgtc	gatgtcgtct	ttgctcagag	gccccgagtc	60
gtttggggca	cgtcaagaaa	gtagtcttcg	ctgctgcttg	aagacatgat	caggacacgc	120
ggttcgacct	tcgagtgtac	atgatatccg	tagaatttgc	ttgtgactac	caaggcatat	180
gttagttcgt	gcagtggtaa	aagcggcttc	tcttcttcaa	tctgcgaggt	ggagatgcct	240
actatgatcg	tcatccaact	tggtgtctac	aagacgaaca	caagcttagt	tccgacgaac	300
cagtgaaaac	tctgtaagat	atataagagc	atcaagagtc	ggacttgctt	aggagagtgg	360
atagttgttg	atgctcgcgg	aagctctcat	atagtataga	tatgaagtat	cggtagatcg	420
tagtagtctt	tgtattatat	aggagagggc	tgaatggtgt	gggtcatgat	aatttccaca	480
taatagcgat	taaagcccta	gatcgagggt	atcttgaggc	ataaatgata	gtatcagtgg	540
acatatcctg	agatgaggat	gatatgagat	gatagagatg	aggaagaaag	aggaaagaga	600
gaggcaagaa	cagagatttt	tatacctttg	cagagcagcc	catccgtcac	tgaattcagg	660
catcttcact	ccatactatc	acgagtcaac	gtgaagttgt	ataagcgtag	tgacaggccg	720
cagtgacgat	gatccgtcac	tgcggtggct	atccgcgact	gatcttgcta	tccgtgactg	780
cgttgactct	ggtgaaccaa	gtgttcggga	aggggtgaaa	atgaagctga	agcgggtcag	840
ggaacattcc	aagcaacact	agacgagtc	gcgacgagtc	agcgatccac	tcggtctcac	900
acgctcccaa	tagtctcaat	ttggtgccaa	tggcaactaa	gtattccatc	cacttttaat	960
taaagtgatc	agcgggtcac	gaattcacat	gctggatctg	gtacagatca	gattaatatc	1020
tcctggaata	cgatgaaggc	ccacctcagg	attcacgata	aatttctggt	gactgccagc	1080
tcgaatggca	ttctccgtca	ctctacacct	gccgttggtt	aatttctccga	acctctaatt	1140
gtcaatttct	gccaaaatgc	gtctatcatc	gctggccctg	gcattccagc	ccatcctacc	1200
cgccttaggc	tacagcatca	acgacttctc	ctgcaatagc	accgaacacc	cgaatccagt	1260
tgtgctccta	catgggctag	gcgccaccta	ctacgaagac	ttgaattacc	tgcaagggtg	1320

21078WO.ST25.txt

```

gctacagacc caaggctatt gcacttacgc caaaacctac ggtgcatatg aaggcttccc 1380
ctttgtcggc ggcctcaagg ccatcgccga atcggccacg gaaatcgccg cgtacatccg 1440
cgaggtgaaa gaaaagacgg gcgccgacaa gattgacctt gtcggtcact ccgaaggcgc 1500
cttcagacc ctctacgtcc ctaagttcga ggatggtatc tcggagatgc tggataagct 1560
ggtggccatt gcacctccca ccagaggcac caacttggcg gggatctatg acatcgcata 1620
tgttctggga aatctatcgc gcgatctgat aggcgacgtc ctggataccg tgggctgcgc 1680
cgcctgtgat gatctgggtc cggatggagc agcgattgac cgcttgaacg atggcgagcc 1740
tatcgtgcag ccgggaaata atctaaccgt gattgcatcg cgggccgacg aattggtcac 1800
cccaaccacc acctccttcg tgcatagaaga tggggtgacc aatgaatggg tgcaagacac 1860
ttgtcctcta gacctgtcg gtcataatcgg tgaggcatac gatctgaacg tctggaatct 1920
ggtcaaaaac gccttggact ctacgccgaa gcgtgagttc gtctgctcgc tgggatctcc 1980
cggcaggtga gactatcatc ttctgaaaat ttgtatataa gcatttatat ttggataccc 2040
ggttaccagt cattagtgtc ataattgtata ataatatcac cacaacttcc tccaagc 2097

```

<210> 14

<211> 834

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(834)

<400> 14

```

atg cgt cta tca tcg ctg gcc ctg gca tcc agc gcc atc cta ccc gcc 48
Met Arg Leu Ser Ser Leu Ala Leu Ala Ser Ser Ala Ile Leu Pro Ala
1 5 10 15
tta ggc tac agc atc aac gac ttc tcc tgc aat agc acc gaa cac ccg 96
Leu Gly Tyr Ser Ile Asn Asp Phe Ser Cys Asn Ser Thr Glu His Pro
20 25 30
aat cca gtt gtg ctc cta cat ggg cta ggc gcc acc tac tac gaa gac 144
Asn Pro Val Val Leu Leu His Gly Leu Gly Ala Thr Tyr Tyr Glu Asp
35 40 45
ttg aat tac ctg caa ggt tgg cta cag acc caa ggc tat tgc act tac 192
Leu Asn Tyr Leu Gln Gly Trp Leu Gln Thr Gln Gly Tyr Cys Thr Tyr
50 55 60
gcc aaa acc tac ggt gca tat gaa ggc ttc ccc ttt gtc ggc ggc ctc 240
Ala Lys Thr Tyr Gly Ala Tyr Glu Gly Phe Pro Phe Val Gly Gly Leu
65 70 75 80
aag gcc atc gcc gaa tcg gcc acg gaa atc gcc gcg tac atc cgc gag 288
Lys Ala Ile Ala Glu Ser Ala Thr Glu Ile Ala Ala Tyr Ile Arg Glu
85 90 95
gtg aaa gaa aag acg ggc gcc gac aag att gac ctt gtc ggt cac tcc 336

```

21078WO.ST25.txt

Val	Lys	Glu	Lys	Thr	Gly	Ala	Asp	Lys	Ile	Asp	Leu	Val	Gly	His	Ser		
			100					105					110				
gaa	ggc	gcc	ttc	cag	acc	ctc	tac	gtc	cct	aag	ttc	gag	gat	ggt	atc	384	
Glu	Gly	Ala	Phe	Gln	Thr	Leu	Tyr	Val	Pro	Lys	Phe	Glu	Asp	Gly	Ile		
		115					120					125					
tcg	gag	atg	ctg	gat	aag	ctg	gtg	gcc	att	gca	cct	ccc	acc	aga	ggc	432	
Ser	Glu	Met	Leu	Asp	Lys	Leu	Val	Ala	Ile	Ala	Pro	Pro	Thr	Arg	Gly		
		130				135					140						
acc	aac	ttg	gcg	ggg	atc	tat	gac	atc	gca	tat	gtt	ctg	gga	aac	cta	480	
Thr	Asn	Leu	Ala	Gly	Ile	Tyr	Asp	Ile	Ala	Tyr	Val	Leu	Gly	Asn	Leu		
145					150				155					160			
tcg	cgc	gat	ctg	ata	ggc	gac	gtc	ctg	gat	acc	gtg	ggc	tgc	gcc	gcc	528	
Ser	Arg	Asp	Leu	Ile	Gly	Asp	Val	Leu	Asp	Thr	Val	Gly	Cys	Ala	Ala		
			165				170					175					
tgt	gat	gat	ctg	ggt	ccg	gat	gga	gca	gcg	att	gac	cgc	ttg	aac	gat	576	
Cys	Asp	Asp	Leu	Gly	Pro	Asp	Gly	Ala	Ala	Ile	Asp	Arg	Leu	Asn	Asp		
			180				185					190					
ggc	gag	cct	atc	gtg	cag	ccg	gga	aat	aat	cta	acg	gtg	att	gca	tcg	624	
Gly	Glu	Pro	Ile	Val	Gln	Pro	Gly	Asn	Asn	Leu	Thr	Val	Ile	Ala	Ser		
		195				200					205						
cgg	tcc	gac	gaa	ttg	gtc	acc	cca	acc	acc	acc	tcc	ttc	gtg	cat	gaa	672	
Arg	Ser	Asp	Glu	Leu	Val	Thr	Pro	Thr	Thr	Thr	Ser	Phe	Val	His	Glu		
		210				215					220						
gat	ggg	gtg	acc	aat	gaa	tgg	gtg	caa	gac	act	tgt	cct	cta	gac	cct	720	
Asp	Gly	Val	Thr	Asn	Glu	Trp	Val	Gln	Asp	Thr	Cys	Pro	Leu	Asp	Pro		
225					230				235				240				
gtc	ggt	cat	atc	ggt	gag	gca	tac	gat	ctg	aac	gtc	tgg	aat	ttg	gtc	768	
Val	Gly	His	Ile	Gly	Glu	Ala	Tyr	Asp	Leu	Asn	Val	Trp	Asn	Leu	Val		
			245					250				255					
aaa	aac	gcc	ttg	gac	tct	acg	ccg	aag	cgt	gag	ttc	gtc	tgc	tcg	ctg	816	
Lys	Asn	Ala	Leu	Asp	Ser	Thr	Pro	Lys	Arg	Glu	Phe	Val	Cys	Ser	Leu		
		260					265					270					
gga	tct	ccc	ggc	agg	tga											834	
Gly	Ser	Pro	Gly	Arg													
		275															

<210> 15

<211> 277

<212> PRT

<213> Aspergillus niger

<400> 15

Met Arg Leu Ser Ser Leu Ala Leu Ala Ser Ser Ala Ile Leu Pro Ala

21078W0.ST25.txt

```

1           5           10           15
Leu Gly Tyr Ser Ile Asn Asp Phe Ser Cys Asn Ser Thr Glu His Pro
           20           25           30
Asn Pro Val Val Leu Leu His Gly Leu Gly Ala Thr Tyr Tyr Glu Asp
           35           40           45
Leu Asn Tyr Leu Gln Gly Trp Leu Gln Thr Gln Gly Tyr Cys Thr Tyr
           50           55           60
Ala Lys Thr Tyr Gly Ala Tyr Glu Gly Phe Pro Phe Val Gly Gly Leu
65           70           75           80
Lys Ala Ile Ala Glu Ser Ala Thr Glu Ile Ala Ala Tyr Ile Arg Glu
           85           90           95
Val Lys Glu Lys Thr Gly Ala Asp Lys Ile Asp Leu Val Gly His Ser
           100          105          110
Glu Gly Ala Phe Gln Thr Leu Tyr Val Pro Lys Phe Glu Asp Gly Ile
           115          120          125
Ser Glu Met Leu Asp Lys Leu Val Ala Ile Ala Pro Pro Thr Arg Gly
           130          135          140
Thr Asn Leu Ala Gly Ile Tyr Asp Ile Ala Tyr Val Leu Gly Asn Leu
145          150          155          160
Ser Arg Asp Leu Ile Gly Asp Val Leu Asp Thr Val Gly Cys Ala Ala
           165          170          175
Cys Asp Asp Leu Gly Pro Asp Gly Ala Ala Ile Asp Arg Leu Asn Asp
           180          185          190
Gly Glu Pro Ile Val Gln Pro Gly Asn Asn Leu Thr Val Ile Ala Ser
           195          200          205
Arg Ser Asp Glu Leu Val Thr Pro Thr Thr Thr Ser Phe Val His Glu
           210          215          220
Asp Gly Val Thr Asn Glu Trp Val Gln Asp Thr Cys Pro Leu Asp Pro
225          230          235          240
Val Gly His Ile Gly Glu Ala Tyr Asp Leu Asn Val Trp Asn Leu Val
           245          250          255
Lys Asn Ala Leu Asp Ser Thr Pro Lys Arg Glu Phe Val Cys Ser Leu
           260          265          270
Gly Ser Pro Gly Arg
           275

```

<210> 16

<211> 1881

<212> DNA

<213> *Aspergillus niger*

<400> 16 .

ccgagtgatc cgcgacttct gggtcagctt tggtctgcgg gctccaccag tgccgtcatc

60

21078WO.ST25.txt

```

gcacgcgaga cccgccccgg atgcttagct gaagccggca tagtccatcc ccgctcgggc 120
gtgatgcccc acggtcactg gaggagaggt gcagggagga tgccgttgca tgaatcaagc 180
ccgggggtttg actttcatcc gctcgtttcc tactggcggg ttccgccctct ccatcgaagc 240
cacggatcct tccatccgga tcctggcaga acagtgagga agcagagctt ggttatagta 300
gaaattatta ataccgagct ggtctgcccc tttttcccaa accttccctc tttccatccc 360
tctcgccctcg caccctctt atcctccctc ccgccatgta tatccctcg gtgctgcttc 420
tggccgcgag cctgttccat ggcgcaacgg cgctgccac gcccggtcc acgccatcc 480
cgcccagcca ggatccctgg tacagtgcgc ccgagggctt cgaggaggct gatcccgggtg 540
ccatcctgcg cgtgcggccc gcgccggca acttgaccgt ggtagtgggc aatgcgtcgg 600
cggcctacaa catcctctac cgcactacag acagtcagta caagccctcc tgggctgtga 660
ccaccctgct ggtgcccccc gtggccgcct ccgcccgct caaccagagt gtcctgctct 720
cccaccagat cgcctacgat tcgttcgacg tcaatgccag tcccagctac gccatgtaca 780
ccagcccgcc ctccgatatt atcctcgccc tgcagcgcgg ctggttcggt aacgtccccg 840
attacgaggg ccccaatgcc tctttaccg ccggtgtgca gtccggccat gccaccctcg 900
actcgggtccg cagcgtgctc gcctccgat tcggcctgaa cgaggacgcc cagtacgctc 960
tgtgggggta ctctggcggg gccttgcca gcgaatgggc tgctgaactg cagatgcaat 1020
acgctcccga gttgaacatt gccggtctgg ccgtgggtgg tctcactccc aatgttacca 1080
gcgtcatgga cacggtgacc tcgacctca gtgcgggact catccccgcc gccgccctgg 1140
gtctgtcgag ccagcacccc gagacctac agttcatcct cagccagctc aagacgacgg 1200
gaccctacaa ccgcacagga ttcctagccg ccaaggacct gaccctgtcc gaggcgagg 1260
tcttctacgc ctccagaac atcttcgatt actttgtcaa cggatcggcc acgttccagg 1320
cggaggtggt gcagaaggcg ctgaaccagg acggatacat gggctaccat gggttccgc 1380
agatgccggt gctcgcgtac aaggctattc acgatgagat cagtcccatc caggatacgg 1440
atcgcgtgat caagcgctac tgtggtctgg gattgaacat ctgtatgag cggaacacca 1500
tcggtggcca ctcggcagag caggtgaatg gcaacgccag ggcgtggaac tggttgacga 1560
gcattttcga cggaacgtat gcgcagcagt acaagaccga ggggtgcacg atccgcaatg 1620
tactctgaa cacgacttcc tccgtttatt agagaggggg ctgttggtat gtgaataatg 1680
ctgaagatgg ctgtgtatgg acggtccgct ctctgtata gtaatgggct aatgcatgcg 1740
gcttcatgaa catggtacga aagattagat tatgtatata gtgtggaagt ggtaatgatg 1800
atataatata tgtctatgat ctatgttcct gctattctat acaaacgcga ccattcacag 1860
aatgactact ggcacatctg c 1881

```

<210> 17

<211> 1257

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1257)

<400> 17

```

atg tat atc ccc tcg gtg .ctg ctt ctg gcc gcg agc ctg ttc cat ggc 48

```

21078WO.ST25.txt

Met Tyr Ile Pro Ser Val Leu Leu Leu Ala Ala Ser Leu Phe His Gly	
1 5 10 15	
gca acg gcg ctg ccc acg ccc ggc tcc acg ccc atc ccg ccc agc cag	96
Ala Thr Ala Leu Pro Thr Pro Gly Ser Thr Pro Ile Pro Pro Ser Gln	
20 25 30	
gat ccc tgg tac agt gcg ccc gag ggc ttc gag gag gct gat ccc ggt	144
Asp Pro Trp Tyr Ser Ala Pro Glu Gly Phe Glu Glu Ala Asp Pro Gly	
35 40 45	
gcc atc ctg cgc gtg cgg ccc gcg ccc ggc aac ttg acc gtg gta gtg	192
Ala Ile Leu Arg Val Arg Pro Ala Pro Gly Asn Leu Thr Val Val Val	
50 55 60	
ggc aat gcg tcg gcg gcc tac aac atc ctc tac cgc act aca gac agt	240
Gly Asn Ala Ser Ala Ala Tyr Asn Ile Leu Tyr Arg Thr Thr Asp Ser	
65 70 75 80	
cag tac aag ccc tcc tgg gct gtg acc acc ctg ctg gtg ccc ccc gtg	288
Gln Tyr Lys Pro Ser Trp Ala Val Thr Thr Leu Leu Val Pro Pro Val	
85 90 95	
gcc gcc tcc gcc gcc gtc aac cag agt gtc ctg ctc tcc cac cag atc	336
Ala Ala Ser Ala Ala Val Asn Gln Ser Val Leu Leu Ser His Gln Ile	
100 105 110	
gcc tac gat tcg ttc gac gtc aat gcc agt ccc agc tac gcc atg tac	384
Ala Tyr Asp Ser Phe Asp Val Asn Ala Ser Pro Ser Tyr Ala Met Tyr	
115 120 125	
acc agc ccg ccc tcc gat att atc ctc gcc ctg cag cgc ggc tgg ttc	432
Thr Ser Pro Pro Ser Asp Ile Ile Leu Ala Leu Gln Arg Gly Trp Phe	
130 135 140	
gtt aac gtc ccc gat tac gag ggc ccc aat gcc tct ttc acc gcc ggt	480
Val Asn Val Pro Asp Tyr Glu Gly Pro Asn Ala Ser Phe Thr Ala Gly	
145 150 155 160	
gtg cag tcc ggc cat gcc acc ctc gac tcg gtc cgc agc gtg ctc gcc	528
Val Gln Ser Gly His Ala Thr Leu Asp Ser Val Arg Ser Val Leu Ala	
165 170 175	
tcc gga ttc ggc ctg aac gag gac gcc cag tac gct ctg tgg ggt tac	576
Ser Gly Phe Gly Leu Asn Glu Asp Ala Gln Tyr Ala Leu Trp Gly Tyr	
180 185 190	
tct ggc ggt gcc ttg gcc agc gaa tgg gct gct gaa ctg cag atg caa	624
Ser Gly Gly Ala Leu Ala Ser Glu Trp Ala Ala Glu Leu Gln Met Gln	
195 200 205	
tac gct ccc gag ttg aac att gcc ggt ctg gcc gtg ggt ggt ctc act	672
Tyr Ala Pro Glu Leu Asn Ile Ala Gly Leu Ala Val Gly Gly Leu Thr	
210 215 220	
ccc aat gtt acc agc gtc atg gac acg gtg acc tcg acc atc agt gcg	720
Pro Asn Val Thr Ser Val Met Asp Thr Val Thr Ser Thr Ile Ser Ala	
225 230 235 240	

21078W0.ST25.txt

gga ctc atc ccc gcc gcc gcc ctg ggt ctg tcg agc cag cac ccc gag	768
Gly Leu Ile Pro Ala Ala Ala Leu Gly Leu Ser Ser Gln His Pro Glu	
245 250 255	
acc tac gag ttc atc ctc agc cag ctc aag acg acg gga ccc tac aac	816
Thr Tyr Glu Phe Ile Leu Ser Gln Leu Lys Thr Thr Gly Pro Tyr Asn	
260 265 270	
cgc aca gga ttc cta gcc gcc aag gac ctg acc ctg tcc gag gcg gag	864
Arg Thr Gly Phe Leu Ala Ala Lys Asp Leu Thr Leu Ser Glu Ala Glu	
275 280 285	
gtc ttc tac gcc ttc cag aac atc ttc gat tac ttt gtc aac gga tcg	912
Val Phe Tyr Ala Phe Gln Asn Ile Phe Asp Tyr Phe Val Asn Gly Ser	
290 295 300	
gcc acg ttc cag gcg gag gtg gtg cag aag gcg ctg aac cag gac gga	960
Ala Thr Phe Gln Ala Glu Val Val Gln Lys Ala Leu Asn Gln Asp Gly	
305 310 315 320	
tac atg ggc tac cat ggg ttc ccg cag atg ccg gtg ctc gcg tac aag	1008
Tyr Met Gly Tyr His Gly Phe Pro Gln Met Pro Val Leu Ala Tyr Lys	
325 330 335	
gct att cac gat gag atc agt ccc atc cag gat acg gat cgc gtg atc	1056
Ala Ile His Asp Glu Ile Ser Pro Ile Gln Asp Thr Asp Arg Val Ile	
340 345 350	
aag cgc tac tgt ggt ctg gga ttg aac atc ttg tat gag cgg aac acc	1104
Lys Arg Tyr Cys Gly Leu Gly Leu Asn Ile Leu Tyr Glu Arg Asn Thr	
355 360 365	
atc ggt ggc cac tcg gca gag cag gtg aat ggc aac gcc agg gcg tgg	1152
Ile Gly Gly His Ser Ala Glu Gln Val Asn Gly Asn Ala Arg Ala Trp	
370 375 380	
aac tgg ttg acg agc att ttc gac gga acg tat gcg cag cag tac aag	1200
Asn Trp Leu Thr Ser Ile Phe Asp Gly Thr Tyr Ala Gln Gln Tyr Lys	
385 390 395 400	
acc gag ggg tgc acg atc cgc aat gtc act ctg aac acg act tcc tcc	1248
Thr Glu Gly Cys Thr Ile Arg Asn Val Thr Leu Asn Thr Thr Ser Ser	
405 410 415	
gtt tat tag	1257
Val Tyr	

<210> 18

<211> 418

<212> PRT

<213> Aspergillus niger

<400> 18

Met Tyr Ile Pro Ser Val Leu Leu Leu Ala Ala Ser Leu Phe His Gly

21078W0.ST25.txt

```

1           5           10           15
Ala Thr Ala Leu Pro Thr Pro Gly Ser Thr Pro Ile Pro Pro Ser Gln
20           25           30
Asp Pro Trp Tyr Ser Ala Pro Glu Gly Phe Glu Glu Ala Asp Pro Gly
35           40           45
Ala Ile Leu Arg Val Arg Pro Ala Pro Gly Asn Leu Thr Val Val Val
50           55           60
Gly Asn Ala Ser Ala Ala Tyr Asn Ile Leu Tyr Arg Thr Thr Asp Ser
65           70           75           80
Gln Tyr Lys Pro Ser Trp Ala Val Thr Thr Leu Leu Val Pro Pro Val
85           90           95
Ala Ala Ser Ala Ala Val Asn Gln Ser Val Leu Leu Ser His Gln Ile
100          105          110
Ala Tyr Asp Ser Phe Asp Val Asn Ala Ser Pro Ser Tyr Ala Met Tyr
115          120          125
Thr Ser Pro Pro Ser Asp Ile Ile Leu Ala Leu Gln Arg Gly Trp Phe
130          135          140
Val Asn Val Pro Asp Tyr Glu Gly Pro Asn Ala Ser Phe Thr Ala Gly
145          150          155          160
Val Gln Ser Gly His Ala Thr Leu Asp Ser Val Arg Ser Val Leu Ala
165          170          175
Ser Gly Phe Gly Leu Asn Glu Asp Ala Gln Tyr Ala Leu Trp Gly Tyr
180          185          190
Ser Gly Gly Ala Leu Ala Ser Glu Trp Ala Ala Glu Leu Gln Met Gln
195          200          205
Tyr Ala Pro Glu Leu Asn Ile Ala Gly Leu Ala Val Gly Gly Leu Thr
210          215          220
Pro Asn Val Thr Ser Val Met Asp Thr Val Thr Ser Thr Ile Ser Ala
225          230          235          240
Gly Leu Ile Pro Ala Ala Ala Leu Gly Leu Ser Ser Gln His Pro Glu
245          250          255
Thr Tyr Glu Phe Ile Leu Ser Gln Leu Lys Thr Thr Gly Pro Tyr Asn
260          265          270
Arg Thr Gly Phe Leu Ala Ala Lys Asp Leu Thr Leu Ser Glu Ala Glu
275          280          285
Val Phe Tyr Ala Phe Gln Asn Ile Phe Asp Tyr Phe Val Asn Gly Ser
290          295          300
Ala Thr Phe Gln Ala Glu Val Val Gln Lys Ala Leu Asn Gln Asp Gly
305          310          315          320
Tyr Met Gly Tyr His Gly Phe Pro Gln Met Pro Val Leu Ala Tyr Lys
325          330          335
Ala Ile His Asp Glu Ile Ser Pro Ile Gln Asp Thr Asp Arg Val Ile
340          345          350
Lys Arg Tyr Cys Gly Leu Gly Leu Asn Ile Leu Tyr Glu Arg Asn Thr

```


21078WO.ST25.txt

355 360 365
 Ile Gly Gly His Ser Ala Glu Gln Val Asn Gly Asn Ala Arg Ala Trp
 370 375 380
 Asn Trp Leu Thr Ser Ile Phe Asp Gly Thr Tyr Ala Gln Gln Tyr Lys
 385 390 395 400
 Thr Glu Gly Cys Thr Ile Arg Asn Val Thr Leu Asn Thr Thr Ser Ser
 405 410 415
 Val Tyr

<210> 19

<211> 2809

<212> DNA

<213> *Aspergillus niger*

<400> 19

agtaatgtat	catttgaaag	atcagtaa	gaaatctgct	gcacaatgca	cgctttgaga	60
acgacgatgc	gaatcgtaga	atgcccaagt	cagtctgcgt	ggtcagacga	gacccataca	120
ttgcatatgt	acaatctagt	agtataatat	gggtgtaa	cccataacct	gataactcata	180
cacactatca	gggcttgggt	acatgagcga	agtagtccca	acaatcaa	aatcatccaa	240
actccaagcc	aaatgccagc	gaaaacaaca	aaagcacaa	atgatgttac	agtgcactag	300
ggaaaccaat	ctgtgtcacc	atcactcagg	acaccagata	taacgaaccc	ccctcacaga	360
ccacgagtct	tctccggatc	catctgcacc	tcataccgc	taatttcctt	gaccgtctca	420
aacgccggct	tgcccgcata	tagctgctgg	gacgagctgg	agccgccgcc	ttccgtcgtc	480
gataccgaga	tgggctgggt	tccgcggaac	cgcttgcgca	tatcgatcag	gccgcgtcta	540
tagaaggaca	aacagttagt	aaccctgatg	acttggcggt	gattgcgttt	tacaagaagg	600
tagcggctct	ttactcactt	gcactcgctg	aatcccttcc	gcaattgctg	gcatacgcatg	660
ggaagctcgt	cgacgtacgg	ctcactcaga	cattcgcggt	gcgagcgccg	ttgcaccatg	720
atgcagtctg	attcttggag	acattggg	agagcatttc	ctgttcatcc	aggtgagatt	780
gattagagag	tgtggagctg	aagctgaagt	tggggacaat	gaggtggtga	tctccgttcg	840
gggatacgtc	gagtatccaa	gccgcaattt	aagagtatgg	taaaggatat	aagggtcaaa	900
cgtactgatc	tcttggcagg	aactcggc	tttggcgaac	aacaatggcc	gaattgctca	960
gccaactgac	aagcaggaac	aataccggtc	tgcggcggcg	gacatctgga	gataatttgt	1020
ctgatcggaa	aacaaactca	accaacgggc	cttgccccgg	attaggtaag	ccatcacatg	1080
aagaaggccc	ccatgacgtc	tggggggaat	cctgacttgc	tgcttggtcc	gcttgattta	1140
tcctcttccc	ctagtcatgc	ggcttgggt	ctttgaagca	ttgcttcggc	gcattatgg	1200
tcactactac	tactgcaggt	gataagtatt	ttagttgggt	gatttgcaaa	ttgtccatcc	1260
cttttcgata	ataggaggtt	tggctttaat	cgatcatggc	cgcggtccgg	tcattggacg	1320
gctgttttgg	ttcaggtatt	tggccctttt	tgggtcgctg	atgttggtat	tgctggaatg	1380
ggttatacat	attatcacat	tctgtctgcg	taagtagtgt	gttcattctc	tggaattgtg	1440
gtctatgtcg	aggggcaaga	gctaactgac	gcagctgaac	ctgttattaa	gttctgttac	1500
gatcgatcca	agactatctt	caacgccttc	attcctcccg	atgaccggc	taagcgcggt	1560
aaagaagaga	aaattgctgc	gtcgggttgc	ctggcgctcg	acttcacgga	tatatgcgcg	1620
ctgttcggat	atgaggcgga	ggaacatatc	gtccagacag	gggatggcta	tctgcttggt	1680

21078WO.ST25.txt

ctgcaccgac	tgccctatcg	gaaaggagag	gaggggagga	agatcaacca	gggcgaaggg	1740
agcatcaaga	agaaggctcg	ctatctccac	catggtctca	tgatgtgcag	tgaagtctgg	1800
atctgtctgt	cagaggagca	gcatgcctt	ccgtttcaat	tagtcgaaag	gggctatgac	1860
gtgtggttgg	ggaacaatag	aggaaacaag	tactcgaaga	agtccgtcaa	gcattcgccc	1920
ctgtcgaacg	agttctggga	cttttcgata	gatcagttct	cgttccatga	tatcccagac	1980
agcatcaagt	atatacctgga	agtgcacagg	cagccctccc	tgtcatacgt	ggggttctcg	2040
cagggaacag	cgcaggcatt	tgcgacgctg	tccattcatc	ctttgttgaa	tcagaagatc	2100
gatgtctttg	tggctctcgc	gccggcaatg	gctccgacag	gtcttccaaa	tcatactcgtg	2160
gactcgctca	tgaaggttc	gccgaacttc	ctgtttctgc	tgtttggcag	acgcagcatc	2220
cttagctcaa	cgacgatgtg	gcagacaatt	ctctacccgc	ctatctttgt	ttggatcatc	2280
gacacgtcac	ttcgcggcct	gttcaattgg	aggtgcaaga	acatcagccg	ctggcagaag	2340
ctggcagggg	acctgcatct	gttttccttc	actagcacca	agtcggtcgt	ccattggttc	2400
cagattattc	ggcaccggaa	tttccagttc	tacgatgacg	aaatccatgc	cccgtcaggt	2460
attgtggcca	gtgagcgatt	ttacaagccg	gtcaagtacc	cgactaagaa	cattaagacg	2520
cccattgtcc	tggtgtatgg	cggtagcgat	agtctcggtg	atatcaacgt	gatgttgtcc	2580
gagctccctc	gcgggaccgt	ggcgaaggaa	atcccgcagt	atgagcattt	agatttcttg	2640
tgggcgcgtg	atgtggacca	attggtattc	aaccatgtct	tcgaagcgct	ggagcgggtac	2700
agctcggaga	atcagaaagg	gacattgatg	gagaaggtta	atggtgccgc	gggcacatat	2760
gtaccgacat	aaagtacgag	gtcctgcacc	aatgaagaca	cgcataatc		2809

<210> 20

<211> 1413

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1413)

<400> 20

atg	gcg	cg	g	gtt	ccg	gtc	att	gga	cg	g	ctg	ttt	tgg	ttc	gag	tat	ttg	48
Met	Ala	Arg	Val	Pro	Val	Ile	Gly	Arg	Leu	Phe	Trp	Phe	Glu	Tyr	Leu			
1				5					10				15					
gcc	ctt	ttt	ggg	tcg	ctg	att	ttg	gta	ttg	ctg	gaa	tgg	gtt	ata	cat			96
Ala	Leu	Phe	Gly	Ser	Leu	Ile	Leu	Val	Leu	Leu	Glu	Trp	Val	Ile	His			
			20					25					30					
att	atc	aca	ttc	tgt	ctg	cct	gaa	cct	gtt	att	aag	ttc	tgt	tac	gat			144
Ile	Ile	Thr	Phe	Cys	Leu	Pro	Glu	Pro	Val	Ile	Lys	Phe	Cys	Tyr	Asp			
		35				40					45							
cga	tcc	aag	act	atc	ttc	aac	gcc	ttc	att	cct	ccc	gat	gac	ccg	gct			192
Arg	Ser	Lys	Thr	Ile	Phe	Asn	Ala	Phe	Ile	Pro	Pro	Asp	Asp	Pro	Ala			
		50				55				60								
aag	cg	g	ggt	aaa	gaa	gag	aaa	att	gct	gcg	tcg	gtt	gct	ctg	gcg	tcg		240

21078W0.ST25.txt

Lys	Arg	Gly	Lys	Glu	Glu	Lys	Ile	Ala	Ala	Ser	Val	Ala	Leu	Ala	Ser		
65				70				75							80		
gac	ttc	acg	gat	ata	tgc	gcg	ctg	ttc	gga	tat	gag	gcg	gag	gaa	cat		288
Asp	Phe	Thr	Asp	Ile	Cys	Ala	Leu	Phe	Gly	Tyr	Glu	Ala	Glu	Glu	His		
				85				90							95		
atc	gtc	cag	aca	ggg	gat	ggc	tat	ctg	ctt	ggt	ctg	cac	cga	ctg	ccc		336
Ile	Val	Gln	Thr	Gly	Asp	Gly	Tyr	Leu	Leu	Gly	Leu	His	Arg	Leu	Pro		
				100				105							110		
tat	cgg	aaa	gga	gag	gag	ggg	agg	aag	atc	aac	cag	ggc	gaa	ggg	agc		384
Tyr	Arg	Lys	Gly	Glu	Glu	Gly	Arg	Lys	Ile	Asn	Gln	Gly	Glu	Gly	Ser		
				115				120							125		
atc	aag	aag	aag	gtc	gtc	tat	ctc	cac	cat	ggt	ctc	atg	atg	tgc	agt		432
Ile	Lys	Lys	Lys	Val	Val	Tyr	Leu	His	His	Gly	Leu	Met	Met	Cys	Ser		
				130				135							140		
gaa	gtc	tgg	atc	tgt	ctg	tca	gag	gag	cag	cga	tgc	ctt	ccg	ttt	caa		480
Glu	Val	Trp	Ile	Cys	Leu	Ser	Glu	Glu	Gln	Arg	Cys	Leu	Pro	Phe	Gln		
				145				150							160		
tta	gtc	gaa	agg	ggc	tat	gac	gtg	tgg	ttg	ggg	aac	aat	aga	gga	aac		528
Leu	Val	Glu	Arg	Gly	Tyr	Asp	Val	Trp	Leu	Gly	Asn	Asn	Arg	Gly	Asn		
				165				170							175		
aag	tac	tcg	aag	aag	tcc	gtc	aag	cat	tcg	ccc	ctg	tcg	aac	gag	ttc		576
Lys	Tyr	Ser	Lys	Lys	Ser	Val	Lys	His	Ser	Pro	Leu	Ser	Asn	Glu	Phe		
				180				185							190		
tgg	gac	ttt	tcg	atc	gat	cag	ttc	tcg	ttc	cat	gat	atc	cca	gac	agc		624
Trp	Asp	Phe	Ser	Ile	Asp	Gln	Phe	Ser	Phe	His	Asp	Ile	Pro	Asp	Ser		
				195				200							205		
atc	aag	tat	atc	ctg	gaa	gtg	aca	ggg	cag	ccc	tcc	ctg	tca	tac	gtg		672
Ile	Lys	Tyr	Ile	Leu	Glu	Val	Thr	Gly	Gln	Pro	Ser	Leu	Ser	Tyr	Val		
				210				215							220		
ggg	ttc	tcg	cag	gga	aca	gcg	cag	gca	ttt	gcg	acg	ctg	tcc	att	cat		720
Gly	Phe	Ser	Gln	Gly	Thr	Ala	Gln	Ala	Phe	Ala	Thr	Leu	Ser	Ile	His		
				225				230							240		
cct	ttg	ttg	aat	cag	aag	atc	gat	gtc	ttt	gtg	gct	ctc	gcg	ccg	gca		768
Pro	Leu	Leu	Asn	Gln	Lys	Ile	Asp	Val	Phe	Val	Ala	Leu	Ala	Pro	Ala		
				245				250							255		
atg	gct	ccg	aca	ggt	ctt	cca	aat	cat	ctc	gtg	gac	tcg	ctc	atg	aag		816
Met	Ala	Pro	Thr	Gly	Leu	Pro	Asn	His	Leu	Val	Asp	Ser	Leu	Met	Lys		
				260				265							270		
gct	tcg	ccg	aac	ttc	ctg	ttt	ctg	ctg	ttt	ggc	aga	cgc	agc	atc	ctt		864
Ala	Ser	Pro	Asn	Phe	Leu	Phe	Leu	Leu	Phe	Gly	Arg	Arg	Ser	Ile	Leu		
				275				280							285		
agc	tca	acg	acg	atg	tgg	cag	aca	att	ctc	tac	ccg	cct	atc	ttt	gtt		912
Ser	Ser	Thr	Thr	Met	Trp	Gln	Thr	Ile	Leu	Tyr	Pro	Pro	Ile	Phe	Val		
				290				295							300		

21078WO.ST25.txt

20 25 30
 Ile Ile Thr Phe Cys Leu Pro Glu Pro Val Ile Lys Phe Cys Tyr Asp
 35 40 45
 Arg Ser Lys Thr Ile Phe Asn Ala Phe Ile Pro Pro Asp Asp Pro Ala
 50 55 60
 Lys Arg Gly Lys Glu Glu Lys Ile Ala Ala Ser Val Ala Leu Ala Ser
 65 70 75 80
 Asp Phe Thr Asp Ile Cys Ala Leu Phe Gly Tyr Glu Ala Glu Glu His
 85 90 95
 Ile Val Gln Thr Gly Asp Gly Tyr Leu Leu Gly Leu His Arg Leu Pro
 100 105 110
 Tyr Arg Lys Gly Glu Glu Gly Arg Lys Ile Asn Gln Gly Glu Gly Ser
 115 120 125
 Ile Lys Lys Lys Val Val Tyr Leu His His Gly Leu Met Met Cys Ser
 130 135 140
 Glu Val Trp Ile Cys Leu Ser Glu Glu Gln Arg Cys Leu Pro Phe Gln
 145 150 155 160
 Leu Val Glu Arg Gly Tyr Asp Val Trp Leu Gly Asn Asn Arg Gly Asn
 165 170 175
 Lys Tyr Ser Lys Lys Ser Val Lys His Ser Pro Leu Ser Asn Glu Phe
 180 185 190
 Trp Asp Phe Ser Ile Asp Gln Phe Ser Phe His Asp Ile Pro Asp Ser
 195 200 205
 Ile Lys Tyr Ile Leu Glu Val Thr Gly Gln Pro Ser Leu Ser Tyr Val
 210 215 220
 Gly Phe Ser Gln Gly Thr Ala Gln Ala Phe Ala Thr Leu Ser Ile His
 225 230 235 240
 Pro Leu Leu Asn Gln Lys Ile Asp Val Phe Val Ala Leu Ala Pro Ala
 245 250 255
 Met Ala Pro Thr Gly Leu Pro Asn His Leu Val Asp Ser Leu Met Lys
 260 265 270
 Ala Ser Pro Asn Phe Leu Phe Leu Leu Phe Gly Arg Arg Ser Ile Leu
 275 280 285
 Ser Ser Thr Thr Met Trp Gln Thr Ile Leu Tyr Pro Pro Ile Phe Val
 290 295 300
 Trp Ile Ile Asp Thr Ser Leu Arg Gly Leu Phe Asn Trp Arg Cys Lys
 305 310 315 320
 Asn Ile Ser Arg Trp Gln Lys Leu Ala Gly Tyr Leu His Leu Phe Ser
 325 330 335
 Phe Thr Ser Thr Lys Ser Val Val His Trp Phe Gln Ile Ile Arg His
 340 345 350
 Arg Asn Phe Gln Phe Tyr Asp Asp Glu Ile His Ala Pro Leu Ser Ile
 355 360 365
 Val Ala Ser Glu Arg Phe Tyr Lys Pro Val Lys Tyr Pro Thr Lys Asn

21078WO.ST25.txt

370 375 380
 Ile Lys Thr Pro Ile Val Leu Leu Tyr Gly Gly Ser Asp Ser Leu Val
 385 390 395 400
 Asp Ile Asn Val Met Leu Ser Glu Leu Pro Arg Gly Thr Val Ala Lys
 405 410 415
 Glu Ile Pro Gln Tyr Glu His Leu Asp Phe Leu Trp Ala Arg Asp Val
 420 425 430
 Asp Gln Leu Val Phe Asn His Val Phe Glu Ala Leu Glu Arg Tyr Ser
 435 440 445
 Ser Glu Asn Gln Lys Gly Thr Leu Met Glu Lys Val Asn Gly Ala Ala
 450 455 460
 Gly Thr Tyr Val Pro Thr
 465 470

<210> 22

<211> 3328

<212> DNA

<213> *Aspergillus niger*

<400> 22

gatttatgaa	gacaggggag	ctctcagtag	atgatcttcg	cacaattgca	cttcctgggg	60
agcctgttta	gtctctagt	aattattgat	agacaggtca	tctgcctcga	gggggttcta	120
ctaacaacgt	gatatctatg	ttgctccttt	actttagaag	aaagggttctg	cttggtagct	180
ggaaccagat	atatagttga	tgtgagtata	tgaagattcc	aatgctttgg	aatattccgc	240
cgtggctgaa	tgatgggact	ctcactgcca	agccaaggga	ttcctcccga	aatttttgca	300
catatgttgt	tgatgcctta	tccctctggc	attcactcgt	tgctgcctcg	gggtgggaccc	360
gacagtcctc	aaacgatgaa	atcttattgg	ctctgctagt	tgagctcggt	ttcaccattt	420
ctattggcgc	tttctcactc	tactccatat	tacagcttcc	gctttgcaat	gcggggctgt	480
gctgcgactt	tgaattgctc	gcatagcaag	agacactgac	cagcaatcca	gctcttctgc	540
ccacatatgt	tgcttttgcc	ttagtatctc	ataatttatg	tgtccagtga	gacagtttgt	600
ttgtactgta	gcttgagttg	ggaatcgtgt	cctgtgacca	tggaatatata	tattctggat	660
ctcagaacat	ctctaccggt	tgtaattttt	gatatacttc	ccaggatggg	acaatgggga	720
cgatgagtat	tgggatgcca	tatcacttga	aagcctctta	gacagactgc	acctattttt	780
attatgctaa	attcttttacg	agacactttc	ttcaagtttc	tgcccttttg	tgaggcagag	840
tgaaacacga	gcgttcaaac	ttgtgttgta	gatgtttatg	atatttatct	cagacagtct	900
ttccacatcc	tgtaatcccc	aacagaaaaa	gatacacagt	atatcactag	aagctcctaa	960
tagttatcat	gctgcaccct	aacagcaatg	cagtcaccct	gctgcgtcag	cgaccccgat	1020
tccggagaag	tatccgagat	agcgataagg	atgcggagat	aagattggca	agtggagatg	1080
agaaagatat	cctcggcctc	agaagtaggc	ccgatgataa	ataactagt	aacaagtcce	1140
ccgcccttct	ccgagcaaac	tacacttcaa	catgctgaat	gcacgctcca	ttgctctggc	1200
ctcgttgcca	gttcttctcc	tactattcgc	ccagcaactt	gcctctcacc	caaccgagca	1260
gattcaagcc	attctggctc	cgtgggtccc	ggccgcacta	caagatgtcg	tgctctataa	1320
tcgacctcgc	gtcataatcc	cccagggcac	tgctgctcggc	acgaccttga	cagacacgct	1380

21078W0.ST25.txt

caagtccccg	gtagatgctt	tccgaggaat	tccatacgca	ttgcctccaa	ttggggatag	1440
acggtttcgc	cgtgcggagg	ctgtccatgc	gacggacgag	attatcgatg	ctagtgaatt	1500
cggcccaagg	tatgcttctt	atacgacatt	cagatcatat	ctgacctttc	aggtgccctg	1560
gaaagcagct	cttgaatcca	aatgacatag	gtggtgatga	agactgtctc	acagtcaatg	1620
tcttccggcc	tcatggcgct	cagggaaaac	tccctgtcgc	tgtatacgtg	cacggcggag	1680
cctacaatcg	cggcactggg	aggtgtatca	ccctcagtcc	tctatatacc	cacagctaaa	1740
tatccagcct	ccggacacaa	cacggcctcg	atggtcggct	ggtcggacga	gcccttcggt	1800
gcagtcagct	tcaactaccg	gtacgtcctc	aaacctgtcc	tccgaatcaa	ctcaactaac	1860
aaacctatcag	catcggcgcc	ctcggcttcc	tcccatccac	cctaaccgcc	aaagaaggaa	1920
tcctcaacct	aggcctccat	gaccagatcc	tcctgctgca	atgggtccaa	gaaaacatcg	1980
cacattttcaa	cggcgaccca	acccaagtca	ctctaactcg	cctctccgcc	ggcgcgcact	2040
ccgtatgccc	ccttctaaga	tacaaataga	actcagtccc	ctacccccaa	actaacgcca	2100
cacagatagc	ccaccacatc	atgaactaca	accacacaaa	cacccccctc	tttcaccgcg	2160
ccatcatcga	atccggcgcc	gccacctccc	gcgcggtcca	cccctacaac	gcctccctcc	2220
acgaatccca	attcacagac	ttcctcactg	aaacgggctg	cactaacctc	cccgcactcg	2280
ccattttgcc	ctgtctccgc	gccctcccat	cctcagccat	taccaccgcc	tccatctccg	2340
tcttcgacaa	atacaacccc	tccatccgct	gggccttcca	accggtcatc	gaccacgaga	2400
tcattccaccg	ccggcccatc	gacgcctggc	gctcaggaaa	gtggaatagg	atgcccatcc	2460
taacgggctt	caactcgaac	gaggggacat	actacgtccc	tcgcaacctc	tctctctccg	2520
aggatttcac	ttcgttcttc	cgaacctctc	tccccgcgta	ccccgagagc	gacatccaga	2580
ccatcgatga	gatctacccc	gatccgaatg	tatatgctac	ggcgtcgcca	tacctcgaga	2640
caaggccgat	cccgagtcta	ggaaggcagt	ttaagcggct	ggaggcggcg	tatgggcatt	2700
atgcgtatgc	gtgtccagta	cggcagacgg	cggggtttgt	tgctaatgat	gatggttggtg	2760
gtgagccggt	gtttttgtat	cgctgggcgt	tgaataagac	tgttattgga	ggcgcgaaacc	2820
atggtgatca	gatggagtat	gagacgttta	atcctgcggt	tagggatatt	tcggaggctc	2880
agagggaggt	tgcggggttg	tttcatgcgt	atgtgacttc	gtttgtggtg	catggggatc	2940
cgaatgttct	ggggggtagg	tatgagggga	gggaggtttg	ggagaggtat	agtggggagg	3000
gaggggaggt	gatggtgttt	ggggagggga	atgatgaacg	tgctggggggg	gatggagttg	3060
gggttgccgc	gaggttgaag	agggatgagt	ggggggtgaa	ggagtgtgga	ttttggtctg	3120
ggaggagtgg	gatttccgag	tgatgggttg	tttatatata	gtctagtgga	aggggatgta	3180
tatactgtag	tcactatctg	tagaacttta	cttgggtgtg	agatagtaaa	tactacaact	3240
gctgaagacc	ttgggataga	acgacatgct	gtttaatcct	caacctgac	tagatatatt	3300
gtgcattact	tgcattccacg	cctaacat				3328

<210> 23

<211> 1779

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1779)

21078W0.ST25.txt

<400> 23

atg ctg aat gca cgc tcc att gct ctg gcc tcg ttg cca gtt ctt ctc	48
Met Leu Asn Ala Arg Ser Ile Ala Leu Ala Ser Leu Pro Val Leu Leu	
1 5 10 15	
cta cta ttc gcc cag caa ctt gcc tct cac cca acc gag cag att caa	96
Leu Leu Phe Ala Gln Gln Leu Ala Ser His Pro Thr Glu Gln Ile Gln	
20 25 30	
gcc att ctg gct ccg tgg gtc ccg gcc gca cta caa gat gtc gtg ctc	144
Ala Ile Leu Ala Pro Trp Val Pro Ala Ala Leu Gln Asp Val Val Leu	
35 40 45	
tat aat cga cct cgc gtc ata atc ccc cag ggc act gtc gtc ggc acg	192
Tyr Asn Arg Pro Arg Val Ile Ile Pro Gln Gly Thr Val Val Gly Thr	
50 55 60	
acc ttg aca gac acg ctc aag tcc ccg gta gat gct ttc cga gga att	240
Thr Leu Thr Asp Thr Leu Lys Ser Pro Val Asp Ala Phe Arg Gly Ile	
65 70 75 80	
cca tac gca ttg cct cca att ggg gat aga cgg ttt cgc cgt gcg gag	288
Pro Tyr Ala Leu Pro Pro Ile Gly Asp Arg Arg Phe Arg Arg Ala Glu	
85 90 95	
gct gtc cat gcg acg gac gag att atc gat gct agt gaa ttc ggc cca	336
Ala Val His Ala Thr Asp Glu Ile Ile Asp Ala Ser Glu Phe Gly Pro	
100 105 110	
agg tgc cct gga aag cag ctc ttg aat cca aat gac ata ggt ggt gat	384
Arg Cys Pro Gly Lys Gln Leu Leu Asn Pro Asn Asp Ile Gly Gly Asp	
115 120 125	
gaa gac tgt ctc aca gtc aat gtc ttc cgg cct cat ggc gct cag gga	432
Glu Asp Cys Leu Thr Val Asn Val Phe Arg Pro His Gly Ala Gln Gly	
130 135 140	
aaa ctc cct gtc gct gta tac gtg cac ggc gga gcc tac aat cgc ggc	480
Lys Leu Pro Val Ala Val Tyr Val His Gly Gly Ala Tyr Asn Arg Gly	
145 150 155 160	
act gct aaa tat cca gcc tcc gga cac aac acg gcc tcg atg gtc ggc	528
Thr Ala Lys Tyr Pro Ala Ser Gly His Asn Thr Ala Ser Met Val Gly	
165 170 175	
tgg tcg gac gag ccc ttc gtt gca gtc agc ttc aac tac cgc atc ggc	576
Trp Ser Asp Glu Pro Phe Val Ala Val Ser Phe Asn Tyr Arg Ile Gly	
180 185 190	
gcc ctc ggc ttc ctc cca tcc acc cta acc gcc aaa gaa gga atc ctc	624
Ala Leu Gly Phe Leu Pro Ser Thr Leu Thr Ala Lys Glu Gly Ile Leu	
195 200 205	
aac cta ggc ctc cat gac cag atc ctc ctg ctg caa tgg gtc caa gaa	672
Asn Leu Gly Leu His Asp Gln Ile Leu Leu Leu Gln Trp Val Gln Glu	
210 215 220	
aac atc gca cat ttc aac ggc gac cca acc caa gtc act cta atc ggc	720

42/71

21078W0.ST25.txt

			85					90				95			
Ala	Val	His	Ala	Thr	Asp	Glu	Ile	Ile	Asp	Ala	Ser	Glu	Phe	Gly	Pro
			100					105				110			
Arg	Cys	Pro	Gly	Lys	Gln	Leu	Leu	Asn	Pro	Asn	Asp	Ile	Gly	Gly	Asp
		115				120						125			
Glu	Asp	Cys	Leu	Thr	Val	Asn	Val	Phe	Arg	Pro	His	Gly	Ala	Gln	Gly
	130					135					140				
Lys	Leu	Pro	Val	Ala	Val	Tyr	Val	His	Gly	Gly	Ala	Tyr	Asn	Arg	Gly
145				150					155					160	
Thr	Ala	Lys	Tyr	Pro	Ala	Ser	Gly	His	Asn	Thr	Ala	Ser	Met	Val	Gly
			165					170						175	
Trp	Ser	Asp	Glu	Pro	Phe	Val	Ala	Val	Ser	Phe	Asn	Tyr	Arg	Ile	Gly
		180						185					190		
Ala	Leu	Gly	Phe	Leu	Pro	Ser	Thr	Leu	Thr	Ala	Lys	Glu	Gly	Ile	Leu
	195					200						205			
Asn	Leu	Gly	Leu	His	Asp	Gln	Ile	Leu	Leu	Leu	Gln	Trp	Val	Gln	Glu
	210					215					220				
Asn	Ile	Ala	His	Phe	Asn	Gly	Asp	Pro	Thr	Gln	Val	Thr	Leu	Ile	Gly
225				230					235					240	
Leu	Ser	Ala	Gly	Ala	His	Ser	Ile	Ala	His	His	Ile	Met	Asn	Tyr	Asn
			245					250					255		
Pro	Pro	Asn	Thr	Pro	Leu	Phe	His	Arg	Ala	Ile	Ile	Glu	Ser	Gly	Ala
		260						265				270			
Ala	Thr	Ser	Arg	Ala	Val	His	Pro	Tyr	Asn	Ala	Ser	Leu	His	Glu	Ser
	275					280						285			
Gln	Phe	Thr	Asp	Phe	Leu	Thr	Glu	Thr	Gly	Cys	Thr	Asn	Leu	Pro	Asp
	290				295						300				
Thr	Ala	Ile	Leu	Pro	Cys	Leu	Arg	Ala	Leu	Pro	Ser	Ser	Ala	Ile	Thr
305				310					315					320	
Thr	Ala	Ser	Ile	Ser	Val	Phe	Asp	Lys	Tyr	Asn	Pro	Ser	Ile	Arg	Trp
			325					330						335	
Ala	Phe	Gln	Pro	Val	Ile	Asp	His	Glu	Ile	Ile	His	Arg	Arg	Pro	Ile
	340					345						350			
Asp	Ala	Trp	Arg	Ser	Gly	Lys	Trp	Asn	Arg	Met	Pro	Ile	Leu	Thr	Gly
	355					360					365				
Phe	Asn	Ser	Asn	Glu	Gly	Thr	Tyr	Tyr	Val	Pro	Arg	Asn	Leu	Ser	Leu
	370				375					380					
Ser	Glu	Asp	Phe	Thr	Ser	Phe	Phe	Arg	Thr	Leu	Leu	Pro	Ala	Tyr	Pro
385				390					395					400	
Glu	Ser	Asp	Ile	Gln	Thr	Ile	Asp	Glu	Ile	Tyr	Pro	Asp	Pro	Asn	Val
			405					410						415	
Tyr	Ala	Thr	Ala	Ser	Pro	Tyr	Leu	Glu	Thr	Arg	Pro	Ile	Pro	Ser	Leu
	420					425						430			
Gly	Arg	Gln	Phe	Lys	Arg	Leu	Glu	Ala	Ala	Tyr	Gly	His	Tyr	Ala	Tyr

21078WO.ST25.txt

435 440 445
 Ala Cys Pro Val Arg Gln Thr Ala Gly Phe Val Ala Asn Asp Asp Gly
 450 455 460
 Cys Gly Glu Pro Val Phe Leu Tyr Arg Trp Ala Leu Asn Lys Thr Val
 465 470 475 480
 Ile Gly Gly Ala Asn His Gly Asp Gln Met Glu Tyr Glu Thr Phe Asn
 485 490 495
 Pro Ala Val Arg Asp Ile Ser Glu Ala Gln Arg Glu Val Ala Gly Leu
 500 505 510
 Phe His Ala Tyr Val Thr Ser Phe Val Val His Gly Asp Pro Asn Val
 515 520 525
 Leu Gly Gly Arg Tyr Glu Gly Arg Glu Val Trp Glu Arg Tyr Ser Gly
 530 535 540
 Glu Gly Gly Glu Val Met Val Phe Gly Glu Gly Asn Asp Glu Arg Ala
 545 550 555 560
 Gly Gly Asp Gly Val Gly Val Ala Ala Arg Leu Lys Arg Asp Glu Trp
 565 570 575
 Gly Val Lys Glu Cys Gly Phe Trp Ser Gly Arg Ser Gly Ile Ser Glu
 580 585 590

<210> 25

<211> 3932

<212> DNA

<213> *Aspergillus niger*

<400> 25

cagataacgt	tttgagtttg	gggatcttga	ttatctcggc	tccaaacaga	ctcgcctatc	60
cgagagatca	agtacataat	gcaactagct	attagtcaaa	tataacgccg	gcagaagtct	120
atthtgcct	tttctctttc	tttcctcgaa	gaaaaccggt	ggattaactt	gagccggtcg	180
gcctcaaagt	cggctcaacc	ggcgcggtgc	caactttaaa	tgcagacaac	catcggtttcc	240
ggccgttgtg	ggggcgatgt	agatcagatc	caaattccca	aaacatccat	ggggtaaatac	300
aagaattgag	gttacatcga	ccgatagggc	tcttaatcca	accctcttca	cggggaaaac	360
cttctatatg	atacatgggt	tactcctctg	tttctcttcc	tccccggagg	tgccaaatcc	420
gggcgcatcg	tgtctattct	tagcaaccag	cgaatttgac	aaattgatcc	aatcccatag	480
aatcagagta	actctacaac	ccaatcagtc	gcctaatacg	cacagcaaaa	gaagatgcat	540
tcggacagcc	aacgcaagaa	aagagattaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	600
aaaaggcctc	ccctcatcac	ctcaccaaag	tcgcaatcaa	tcagcgacca	ctagctacat	660
cgcgactgaa	cgatagcatt	ccgcatgggt	ttaaagttca	agacagttgc	tatgcttgcc	720
cgaaccttta	cacattcttg	ccctttccgt	agaattccaa	gctcatcgga	cagagagtag	780
tgtttctgtg	aatgtggtgg	tttaccaccg	ttacctctgc	tgtctatcac	ttgtccttac	840
ccctgagcac	aggcaccata	gttacaacac	ccccacgggg	ccattgtctg	ttttcagctt	900
cagcttcgtc	gacaatggac	tgtcatatcc	cctcatctca	aaagaatgtc	ggaaacactg	960
tatggcatgg	cgtgtgggaa	ccgatcaatt	tgtataatat	cttaggccca	cctcttcccc	1020
tccgagaggt	ttgacatcag	ggggtttcag	agatagtccg	tcgatattta	tggcttcctc	1080

21078W0.ST25.txt

tgtcttcttg	ccgctacttg	cggcctcatt	actgcccaca	ctcgcttcta	cacagaatgc	1140
cgatacacg	acatccgctc	ctactgtgca	agtccgcaat	ggcacatacg	agggctctcta	1200
taatcccacg	tacaatcagg	acttgttcct	cggcataccg	tatgcgagc	ctccggttg	1260
tgagctacga	ttccgtccac	cacaaccgct	caacacgacg	tggactggca	ctcgaaatgc	1320
aacagcctat	tacaatgaat	gtatcggtta	tggtagcgac	gactgggtatt	ggaccgacgt	1380
agtctccgaa	gattgtctcg	ctctcagtg	gattcgacct	cacggcatcg	actcaagcgc	1440
gaagctgccc	gtcgtcttct	ggatgcatgg	tggagaattc	gcagaaggag	gcactcgcg	1500
ctcccgttac	aacctctcct	acatcgcca	acaatcccag	gagatgcaat	ctcccatcat	1560
tggcgtgact	gtcaactacc	gcctttcggg	atggggattc	ctctatagcc	aggaagtgc	1620
cgacgaaggc	tccgccaact	taggactccg	cgaccaacgg	cacgctctgt	actggctcca	1680
agagaatatc	gcttccttcg	gcggcgaccc	gtcgcggtc	accatctggg	gccaaagtgc	1740
cggtgccaac	agcgtcggtc	tccatttagt	ggcatacgac	ggccagaatg	atggcatctt	1800
ccgtgccggg	atcgccgaga	gcggctccgt	accctccctc	gcagcataca	tgagcgccga	1860
agatgcacaa	ccatactatg	atgccgtcgt	caacgcaacc	aactgcaccg	gctcttccaa	1920
caccttact	tgtctccgtg	aagttccac	cgacgtcctc	agctccatct	tcaacagctc	1980
cctcgtcgt	ggggcaggat	atcatccgt	cattgacggc	gatttcctca	gagcctcggg	2040
gatagttaat	ctccagactg	gccaattcgc	caaaaccccg	cttcttatcg	gcaccaactt	2100
cgacgaagg	accaagtatg	cccctcatgg	ctataatacc	accgaccaat	ttgtctccct	2160
cgtccaagcc	aacggaacca	attataccag	cgtctcacc	attgcatccc	tgtaccaga	2220
tgaccagcc	gttggtattc	cgggaaccct	tcaaggctgt	ccccaccgt	catacggtta	2280
ccagtgaag	cgcggtggctg	ccttcctcgg	cgatctgctc	atgcacgcgc	ctcgccgcgt	2340
gacaaccag	tggctggcac	actggaatgt	acctgcctac	gtgtatcact	ggaacgtgat	2400
gacactagg	ccattagatg	gagccgcgca	tggctatgaa	gtccccttca	gtttccataa	2460
ttatgatggt	ttgggcgatg	aacggggaaa	cgacagcgtg	acctggccac	aactatcgac	2520
tatgatgtca	cggatgtggg	tgagctttat	taatcatttg	gatccgaatt	atagtaatag	2580
tgagtgattt	gccccaccta	cctctggaca	ctgctttagg	agcttgaggg	taaggaagga	2640
tgctgacacg	ctgctctgct	agtgcggat	atccactggc	ctgtctacac	aacagaaacc	2700
ccgcaaaata	tggcttttga	tgtcaatgtg	actggactgg	cttatgttga	accagatacc	2760
tatagagcgg	aggggaattgc	gtatatcact	agcattctgc	agagtgcctt	taatcggtag	2820
ggtagactag	aggcttcaat	atcaatagat	atcacacata	caggagagca	gcccattgtt	2880
ccctccagat	caagagctat	tccgttaaaa	ggtagtgcac	ccccgcaccg	gggggaaggc	2940
cggggagtg	ttacctctgt	gtgaaactag	aattccagca	acgatgggtt	tagaaaggcc	3000
agatctgttg	actcattgtt	tgatcctccg	atgttgcatc	cgagaaagct	tctgcttggt	3060
cgtgccaaag	atgttaacag	ctgctgttga	ggcaactcta	gaaaccccat	agacctttac	3120
tatctcgctg	actagaggg	acagtaggtc	ctactttgaa	ttccttggcg	gttgggattt	3180
cgcggaagg	tgtctcaacc	ctcaatgctt	gtcacgacag	acggcttggc	aatgagacga	3240
gaccacgggc	gattgacatg	tgtcaagcag	tagctatcgg	gaatctgaaa	aagcatggct	3300
gtcatggact	ttgcaggcaa	aggctgtctg	ttctagacca	tcggctagag	cgcggtgagc	3360
atactaggcg	agctgaaaag	cctagaagcg	gttgccggtt	atccgctttg	tttgtgccct	3420
ttccgtttcc	gggcgtaggc	aatcacattt	aggcaatgcc	gtgtgggcct	tggagatctc	3480
acctaacctt	attgcatttt	acctcacggt	gatacaacct	gagtgactat	cagggaaact	3540
gagcctattg	atcatcacat	attagacca	cacaaagctg	ccaaggaaca	atagtaatgt	3600
gagcgccaag	gagatatctt	tgaactttgt	ctccagatct	tgtactacat	acccagccag	3660
acaggggttc	gtatcgatgg	ctccacagcg	ggatatcatg	aatcttcatg	tcgtcacgac	3720

21078WO.ST25.txt

tcatacctcg agcgataggg ccgggtatta ctccatctgg aaattgtcat gactgtagag	3780
ctcagctgtc cgggatacga gcattatccg tcagtttata aattccaggg ccatacctgct	3840
caatctcaac atgtgggctc ttacgctgtc atcatattag ttaggggtcca agagaatcac	3900
agaatcattg gcattgttct tcatacgttcc aa	3932

<210> 26

<211> 1518

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1518)

<400> 26

atg gct tcc tct gtc ttc ttg ccg cta ctt gcg gcc tca tta ctg ccc	48
Met Ala Ser Ser Val Phe Leu Pro Leu Leu Ala Ala Ser Leu Leu Pro	
1 5 10 15	
aca ctc gct tct aca cag aat gcc gat aca ccg aca tcc gct cct act	96
Thr Leu Ala Ser Thr Gln Asn Ala Asp Thr Pro Thr Ser Ala Pro Thr	
20 25 30	
gtg caa gtc cgc aat ggc aca tac gag ggt ctc tat aat ccc acg tac	144
Val Gln Val Arg Asn Gly Thr Tyr Glu Gly Leu Tyr Asn Pro Thr Tyr	
35 40 45	
aat cag gac ttg ttc ctc ggc ata ccg tat gcg cag cct ccg gtt ggt	192
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly	
50 55 60	
gag cta cga ttc cgt cca cca caa ccg ctc aac acg acg tgg act ggc	240
Glu Leu Arg Phe Arg Pro Pro Gln Pro Leu Asn Thr Thr Trp Thr Gly	
65 70 75 80	
act cga aat gca aca gcc tat tac aat gaa tgt atc ggt tat ggt agc	288
Thr Arg Asn Ala Thr Ala Tyr Tyr Asn Glu Cys Ile Gly Tyr Gly Ser	
85 90 95	
gac gac tgg tat tgg acc gac gta gtc tcc gaa gat tgt ctc gct ctc	336
Asp Asp Trp Tyr Trp Thr Asp Val Val Ser Glu Asp Cys Leu Ala Leu	
100 105 110	
agt gtg att cga cct cac ggc atc gac tca agc gcg aag ctg ccc gtc	384
Ser Val Ile Arg Pro His Gly Ile Asp Ser Ser Ala Lys Leu Pro Val	
115 120 125	
gtc ttc tgg atg cat ggt gga gaa ttc gca gaa gga ggc act cgc gac	432
Val Phe Trp Met His Gly Gly Glu Phe Ala Glu Gly Gly Thr Arg Asp	
130 135 140	
tcc cgt tac aac ctc tcc tac atc gtc caa caa tcc cag gag atg caa	480

Ser	Arg	Tyr	Asn	Leu	Ser	Tyr	Ile	Val	Gln	Gln	Ser	Gln	Glu	Met	Gln	
145					150				155						160	
tct	ccc	atc	att	ggc	gtg	act	gtc	aac	tac	cgc	ctt	tcg	gga	tgg	gga	528
Ser	Pro	Ile	Ile	Gly	Val	Thr	Val	Asn	Tyr	Arg	Leu	Ser	Gly	Trp	Gly	
				165					170						175	
ttc	ctc	tat	agc	cag	gaa	gtc	gcc	gac	gaa	ggc	tcc	gcc	aac	tta	gga	576
Phe	Leu	Tyr	Ser	Gln	Glu	Val	Ala	Asp	Glu	Gly	Ser	Ala	Asn	Leu	Gly	
			180						185					190		
ctc	cgc	gac	caa	cgg	cac	gct	ctg	tac	tgg	ctc	caa	gag	aat	atc	gct	624
Leu	Arg	Asp	Gln	Arg	His	Ala	Leu	Tyr	Trp	Leu	Gln	Glu	Asn	Ile	Ala	
		195					200					205				
tcc	ttc	ggc	ggc	gac	ccg	tcg	cgg	ctc	acc	atc	tgg	ggc	caa	agt	gcc	672
Ser	Phe	Gly	Gly	Asp	Pro	Ser	Arg	Leu	Thr	Ile	Trp	Gly	Gln	Ser	Ala	
	210					215					220					
ggc	gcc	aac	agc	gtc	ggc	ctc	cat	tta	gtg	gca	tac	gac	ggc	cag	aat	720
Gly	Ala	Asn	Ser	Val	Gly	Leu	His	Leu	Val	Ala	Tyr	Asp	Gly	Gln	Asn	
225				230					235						240	
gat	ggc	atc	ttc	cgt	gcc	ggg	atc	gcc	gag	agc	ggc	tcc	gta	ccc	tcc	768
Asp	Gly	Ile	Phe	Arg	Ala	Gly	Ile	Ala	Glu	Ser	Gly	Ser	Val	Pro	Ser	
			245						250					255		
ctc	gca	gca	tac	atg	agc	gcc	gaa	gat	gca	caa	cca	tac	tat	gat	gcc	816
Leu	Ala	Ala	Tyr	Met	Ser	Ala	Glu	Asp	Ala	Gln	Pro	Tyr	Tyr	Asp	Ala	
		260					265					270				
gtc	gtc	aac	gca	acc	aac	tgc	acc	ggc	tct	tcc	aac	acc	ctt	act	tgt	864
Val	Val	Asn	Ala	Thr	Asn	Cys	Thr	Gly	Ser	Ser	Asn	Thr	Leu	Thr	Cys	
		275				280						285				
ctc	cgt	gaa	gtt	ccc	acc	gac	gtc	ctc	agc	tcc	atc	ttc	aac	agc	tcc	912
Leu	Arg	Glu	Val	Pro	Thr	Asp	Val	Leu	Ser	Ser	Ile	Phe	Asn	Ser	Ser	
	290					295				300						
ctc	gtc	gct	ggg	gca	gga	tat	cat	ccc	gtc	att	gac	ggc	gat	ttc	ctc	960
Leu	Val	Ala	Gly	Ala	Gly	Tyr	His	Pro	Val	Ile	Asp	Gly	Asp	Phe	Leu	
305				310					315						320	
aga	gcc	tcg	ggg	ata	gtt	aat	ctc	cag	act	ggc	caa	ttc	gcc	aaa	acc	1008
Arg	Ala	Ser	Gly	Ile	Val	Asn	Leu	Gln	Thr	Gly	Gln	Phe	Ala	Lys	Thr	
			325						330					335		
ccg	ctt	ctt	atc	ggc	acc	aac	ttc	gac	gaa	ggg	acc	aag	tat	gcc	cct	1056
Pro	Leu	Leu	Ile	Gly	Thr	Asn	Phe	Asp	Glu	Gly	Thr	Lys	Tyr	Ala	Pro	
			340					345					350			
cat	ggc	tat	aat	acc	acc	gac	caa	ttt	gtc	tcc	ctc	gtc	caa	gcc	aac	1104
His	Gly	Tyr	Asn	Thr	Thr	Asp	Gln	Phe								

21078W0.ST25.txt

```

gac cca gcc gtt ggt att ccg gga acc ctt caa ggt cgt ccc cca ccg      1200
Asp Pro Ala Val Gly Ile Pro Gly Thr Leu Gln Gly Arg Pro Pro Pro
385          390          395          400
tca tac ggt tac cag tgg aag cgc gtg gct gcc ttc ctc ggc gat ctg      1248
Ser Tyr Gly Tyr Gln Trp Lys Arg Val Ala Ala Phe Leu Gly Asp Leu
          405          410          415
ctc atg cac gcg cct cgc cgc gtg aca acc cag tgg ctg gca cac tgg      1296
Leu Met His Ala Pro Arg Arg Val Thr Thr Gln Trp Leu Ala His Trp
          420          425          430
aat gta cct gcc tac gtg tat cac tgg aac gtg atg aca cta ggg cca      1344
Asn Val Pro Ala Tyr Val Tyr His Trp Asn Val Met Thr Leu Gly Pro
          435          440          445
tta gat gga gcc gcg cat ggc tat gaa gtc ccc ttc agt ttc cat aat      1392
Leu Asp Gly Ala Ala His Gly Tyr Glu Val Pro Phe Ser Phe His Asn
          450          455          460
tat gat ggt ttg ggc gat gaa cgg gga aac gac agc gtg acc tgg cca      1440
Tyr Asp Gly Leu Gly Asp Glu Arg Gly Asn Asp Ser Val Thr Trp Pro
465          470          475          480
caa cta tcg act atg atg tca cgg atg tgg gtg agc ttt att aat cat      1488
Gln Leu Ser Thr Met Met Ser Arg Met Trp Val Ser Phe Ile Asn His
          485          490          495
ttg gat ccg aat tat agt aat agt gag tga      1518
Leu Asp Pro Asn Tyr Ser Asn Ser Glu
          500          505

```

<210> 27

<211> 505

<212> PRT

<213> *Aspergillus niger*

<400> 27

```

Met Ala Ser Ser Val Phe Leu Pro Leu Leu Ala Ala Ser Leu Leu Pro
1          5          10          15
Thr Leu Ala Ser Thr Gln Asn Ala Asp Thr Pro Thr Ser Ala Pro Thr
          20          25          30
Val Gln Val Arg Asn Gly Thr Tyr Glu Gly Leu Tyr Asn Pro Thr Tyr
          35          40          45
Asn Gln Asp Leu Phe Leu Gly Ile Pro Tyr Ala Gln Pro Pro Val Gly
          50          55          60
Glu Leu Arg Phe Arg Pro Pro Gln Pro Leu Asn Thr Thr Trp Thr Gly
65          70          75          80
Thr Arg Asn Ala Thr Ala Tyr Tyr Asn Glu Cys Ile Gly Tyr Gly Ser
          85          90          95

```


21078WO.ST25.txt

Asp Asp Trp Tyr Trp Thr Asp Val Val Ser Glu Asp Cys Leu Ala Leu
 100 105 110
 Ser Val Ile Arg Pro His Gly Ile Asp Ser Ser Ala Lys Leu Pro Val
 115 120 125
 Val Phe Trp Met His Gly Gly Glu Phe Ala Glu Gly Gly Thr Arg Asp
 130 135 140
 Ser Arg Tyr Asn Leu Ser Tyr Ile Val Gln Gln Ser Gln Glu Met Gln
 145 150 155 160
 Ser Pro Ile Ile Gly Val Thr Val Asn Tyr Arg Leu Ser Gly Trp Gly
 165 170 175
 Phe Leu Tyr Ser Gln Glu Val Ala Asp Glu Gly Ser Ala Asn Leu Gly
 180 185 190
 Leu Arg Asp Gln Arg His Ala Leu Tyr Trp Leu Gln Glu Asn Ile Ala
 195 200 205
 Ser Phe Gly Gly Asp Pro Ser Arg Leu Thr Ile Trp Gly Gln Ser Ala
 210 215 220
 Gly Ala Asn Ser Val Gly Leu His Leu Val Ala Tyr Asp Gly Gln Asn
 225 230 235 240
 Asp Gly Ile Phe Arg Ala Gly Ile Ala Glu Ser Gly Ser Val Pro Ser
 245 250 255
 Leu Ala Ala Tyr Met Ser Ala Glu Asp Ala Gln Pro Tyr Tyr Asp Ala
 260 265 270
 Val Val Asn Ala Thr Asn Cys Thr Gly Ser Ser Asn Thr Leu Thr Cys
 275 280 285
 Leu Arg Glu Val Pro Thr Asp Val Leu Ser Ser Ile Phe Asn Ser Ser
 290 295 300
 Leu Val Ala Gly Ala Gly Tyr His Pro Val Ile Asp Gly Asp Phe Leu
 305 310 315 320
 Arg Ala Ser Gly Ile Val Asn Leu Gln Thr Gly Gln Phe Ala Lys Thr
 325 330 335
 Pro Leu Leu Ile Gly Thr Asn Phe Asp Glu Gly Thr Lys Tyr Ala Pro
 340 345 350
 His Gly Tyr Asn Thr Thr Asp Gln Phe Val Ser Leu Val Gln Ala Asn
 355 360 365
 Gly Thr Asn Tyr Thr Ser Ala Leu Thr Ile Ala Ser Leu Tyr Pro Asp
 370 375 380
 Asp Pro Ala Val Gly Ile Pro Gly Thr Leu Gln Gly Arg Pro Pro Pro
 385 390 395 400
 Ser Tyr Gly Tyr Gln Trp Lys Arg Val Ala Ala Phe Leu Gly Asp Leu
 405 410 415
 Leu Met His Ala Pro Arg Arg Val Thr Thr Gln Trp Leu Ala His Trp
 420 425 430
 Asn Val Pro Ala Tyr Val Tyr His Trp Asn Val Met Thr Leu Gly Pro
 435 440 445

21078WO.ST25.txt

Leu Asp Gly Ala Ala His Gly Tyr Glu Val Pro Phe Ser Phe His Asn
 450 455 460
 Tyr Asp Gly Leu Gly Asp Glu Arg Gly Asn Asp Ser Val Thr Trp Pro
 465 470 475 480
 Gln Leu Ser Thr Met Met Ser Arg Met Trp Val Ser Phe Ile Asn His
 485 490 495
 Leu Asp Pro Asn Tyr Ser Asn Ser Glu
 500 505

<210> 28

<211> 3091

<212> DNA

<213> *Aspergillus niger*

<400> 28

```

ggcgaacggg cctgagcgtg cgtcggaggg agaagtagag ccgggactat ggatattggc 60
gaggaatata ttatagtaga ttataggagg tcgaatgcag ctcggtattgg gttgttactt 120
tgagtcagat ggacattggt ggaaaagatg aacgcgcacgg gaaaaaaca tgaggatttg 180
cggggatttc gtcacatgcg gaggcgcgga ttttcccctc cggatttact tcctcaactc 240
tcctttctct ttcatttcca tccgatttga gtccaactca tctcactcga agaatctcat 300
taatttcagg gtctgtctca gccagtcgaa gggttccttag tttcgatcct tcagttggcc 360
cgtcatgtcc attgaccagg aatggagcaa gcccgcgtag ggatcggcca gcggagacaa 420
ctgccaatcc ttggtatcca tacccttaac agcgcaatgg caccagctct ctgccgattc 480
acgtcatctg cacagcctag ctgccgatta ggcttgaccc cttctcactt gcggcatcag 540
tgccgctgat actagcccc acagagtgtt tctcccttcg actgtggctc ggaacgtggg 600
ggcgggttcc aagttcttat gccagaggtt gggttggttag ctttgctcat ctgggtggcc 660
agcacacctc ccatacaata ggatccgtgg tggtggcagg attcttgta tttcgccatg 720
tcgaatcacc gcatgcggaa ggaggacgcc ttgccttgca atgttttctc cacatctgcg 780
accctattgt tcagaccctg gagccgattc cgcgagatgt attcctgccg ggccactgaa 840
agtgccttat aacgtctggg gtgtcctttt attgatgaga gcatgatctt tcgcgttaca 900
gttctcaca tgcggttaaag cattcggtgg cccgaggctc gttgcacaac acaatatgat 960
tttctttcat ctggcaccgt tcttctttct ctttgggtcta gtagtatctt ctcagaaccc 1020
tacggtggac cttggctaca caagatataa aggcaaatct ctgcccaatg gtatcagtca 1080
gtggctgggg atacgctacg cggtgcacc taccgggtct ctgcggttct ctgcgccaca 1140
ggatcctgac acggtagatg gcgttcaaga agcattcaag gtatgggttt ttctacaata 1200
aataaaaaga tatattgcga gtctgtgctt tgctaatacc cagggcacag catggtcccc 1260
ggtgtgttcc caccagccaa tatcccactc ccgcaggcac gtccgaggat tgtctcttcc 1320
tcgatgtata cgctcccagc tcggtggaag ctactacgag gctgcccgtt ttcgtttga 1380
ttcaaggagg cggttcaat gccaaactca gcccacta caatggaaca ggattgatcg 1440
aagcgccaa tatgtccatg gtggtgtca cttcaacta cagggtcggg ccgtacgggt 1500
tcctctctgg atccgaggtg ctggaggag gaagcgtgaa caatggcctg aaggacaaa 1560
tcaaggtcct gaagtgggtg caagagcata tcagcaagg atgcggacac tcaccaaccc 1620
acagcaaatc accgctaatt gcagccgcag tttggaggcg atcccagtca cgttggtatc 1680

```

21078W0.ST25.txt

```

ggcggcgaca gcgcaggcgc agcgtctatc actctccatc tttcagccca cgggtggcaga 1740
gacgacgaac tattccacgc tgccgccgca gagtcccaaa gctttgctcc tatgttgacc 1800
gtcaatcaaa gccaatcgc ctataacaac ctgggtcatcc gcgccggctg cgcaagcgat 1860
tcagacaccc tcgcctgctt acgccgacta aacaccacag aactgcagcg catcaacatc 1920
aacacaccct taccacccgc ccaacaagca cctctctacc tgtacggtec cgtcgtcgac 1980
ggctccctca tcccagacta cacataccgg cttttccagc aaggcaaatt catcaaagtc 2040
cccgtaatct tcggcgacga caccaacgaa ggaacaatct tcgtcccaa aacgacctcc 2100
accgtcggcg aagccgacac cttcatccaa gaccaattcc ccaacatcaa cttcaccac 2160
ctaaccaagc tgaacgactg gtatctcaaa gaaaacaaa ctcgcgagtt cccaattcc 2220
tccccctact gggtcccgcc tagcaccgcg tacggtgaaa tcagatatat ctgtccgggg 2280
atctacatgt cctctgtgtt tgctagtgcc ggtgtcaaca gctggaacta tcattatgct 2340
gtgcaggacc ccgccgcgga agcctcaggc agaggtgtca gtcatactgt ggaagaaaat 2400
gccatttggg gcccgagta tgtgagtggc acaccgccgg cgtcgtatct cactgagaat 2460
gcgccaattg tgccggtgat gcagggctac tggacgagtt tcattagagt gtttgatccg 2520
aatccgctga ggtatccggg gagtccggag tggaagacgt ggagtgatgg acatggggag 2580
gattatcggc ggatatttgt ccgcacgaat gagacgagga tggagacggg gtcggaggcg 2640
cagagggaaa ggtgcgaata ttggagtagt gttgggccgg acttgtcgca gtgattgcac 2700
ttattatctt tggtcggtag taaggatat atatagatag tataatattg taagctatag 2760
agtgatggta cgtgaattga atatatggag aaagatggtc ttgtataaat caaaacattc 2820
ttttttggct gccattccac gatcatcatt cccaatgatc aaaccaagta actataaccg 2880
aatatataca tctatatcaa cctgcttctc atcagaatta ccaaaagacg ggtccggcac 2940
acacagctag accgagcaga tacgtcgaca tgaaccacgg tgatgaaaca taatgcaaca 3000
aaagaagag aaaagaaggc aaaacaagtg agaagcacta ctgctccaca tagagcagta 3060
aacgaacgat gaatgagga tatcatcatc a 3091

```

<210> 29

<211> 1617

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(1617)

<400> 29

```

atg att ttc ttt cat ctg gca ccg ttc ttc ttt ctc ttt ggt cta gta 48
Met Ile Phe Phe His Leu Ala Pro Phe Phe Phe Leu Phe Gly Leu Val
1 5 10 15
gta tct tct cag aac cct acg gtg gac ctt ggc tac aca aga tat aaa 96
Val Ser Ser Gln Asn Pro Thr Val Asp Leu Gly Tyr Thr Arg Tyr Lys
20 25 30
ggc aaa tct ctg ccc aat ggt atc agt cag tgg ctg ggg ata cgc tac 144
Gly Lys Ser Leu Pro Asn Gly Ile Ser Gln Trp Leu Gly Ile Arg Tyr

```

21078WO.ST25.txt

35	40	45	
gcg gct gca cct acc ggg tct ctg cgg ttc tct gcg cca cag gat cct			192
Ala Ala Ala Pro Thr Gly Ser Leu Arg Phe Ser Ala Pro Gln Asp Pro			
50	55	60	
gac acg gta gat ggc gtt caa gaa gca ttc aag cat ggt ccc cgg tgt			240
Asp Thr Val Asp Gly Val Gln Glu Ala Phe Lys His Gly Pro Arg Cys			
65	70	75	80
gtt ccc acc agc caa tat ccc act ccc gca ggc acg tcc gag gat tgt			288
Val Pro Thr Ser Gln Tyr Pro Thr Pro Ala Gly Thr Ser Glu Asp Cys			
85	90	95	
ctc ttc ctc gat gta tac gct ccc agc tcg gtg gaa gct act acg agg			336
Leu Phe Leu Asp Val Tyr Ala Pro Ser Ser Val Glu Ala Thr Thr Arg			
100	105	110	
ctg ccc gtt ttc gtt tgg att caa gga ggc ggc ttc aat gcc aac tcc			384
Leu Pro Val Phe Val Trp Ile Gln Gly Gly Gly Phe Asn Ala Asn Ser			
115	120	125	
agc ccc aac tac aat gga aca gga ttg atc gaa gcg gcc aat atg tcc			432
Ser Pro Asn Tyr Asn Gly Thr Gly Leu Ile Glu Ala Ala Asn Met Ser			
130	135	140	
atg gtg gtg gtc acc ttc aac tac agg gtc ggt ccg tac ggg ttc ctc			480
Met Val Val Val Thr Phe Asn Tyr Arg Val Gly Pro Tyr Gly Phe Leu			
145	150	155	160
tct gga tcc gag gtg ctg gag gga gga agc gtg aac aat ggc ctg aag			528
Ser Gly Ser Glu Val Leu Glu Gly Gly Ser Val Asn Asn Gly Leu Lys			
165	170	175	
gac caa atc aag gtc ctg aag tgg gtg caa gag cat atc agc aag ttt			576
Asp Gln Ile Lys Val Leu Lys Trp Val Gln Glu His Ile Ser Lys Phe			
180	185	190	
gga ggc gat ccc agt cac gtt gtt atc ggc ggc gac agc gca ggc gca			624
Gly Gly Asp Pro Ser His Val Val Ile Gly Gly Asp Ser Ala Gly Ala			
195	200	205	
gcg tct atc act ctc cat ctt tca gcc cac ggt ggc aga gac gac gaa			672
Ala Ser Ile Thr Leu His Leu Ser Ala His Gly Gly Arg Asp Asp Glu			
210	215	220	
cta ttc cac gct gcc gcc gca gag tcc caa agc ttt gct cct atg ttg			720
Leu Phe His Ala Ala Ala Ala Glu Ser Gln Ser Phe Ala Pro Met Leu			
225	230	235	240
acc gtc aat caa agc caa ttc gcc tat aac aac ctg gtc atc cgc gcc			768
Thr Val Asn Gln Ser Gln Phe Ala Tyr Asn Asn Leu Val Ile Arg Ala			
245	250	255	
ggc tgc gca agc gat tca gac acc ctc gcc tgc tta cgc cga cta aac			816
Gly Cys Ala Ser Asp Ser Asp Thr Leu Ala Cys Leu Arg Arg Leu Asn			
260	265	270	
acc aca gaa ctg cag cgc atc aac atc aac aca ccc tta ccc acc gcc			864

21078WO.ST25.txt

Thr	Thr	Glu	Leu	Gln	Arg	Ile	Asn	Ile	Asn	Thr	Pro	Leu	Pro	Thr	Ala	
		275					280					285				
caa	caa	gca	cct	ctc	tac	ctg	tac	ggt	ccc	gtc	gtc	gac	ggc	tcc	ctc	912
Gln	Gln	Ala	Pro	Leu	Tyr	Leu	Tyr	Gly	Pro	Val	Val	Asp	Gly	Ser	Leu	
		290					295					300				
atc	cca	gac	tac	aca	tac	cgg	ctt	ttc	cag	caa	ggc	aaa	ttc	atc	aaa	960
Ile	Pro	Asp	Tyr	Thr	Tyr	Arg	Leu	Phe	Gln	Gln	Gly	Lys	Phe	Ile	Lys	
305					310						315				320	
gtc	ccc	gta	atc	ttc	ggc	gac	gac	acc	aac	gaa	gga	aca	atc	ttc	gtc	1008
Val	Pro	Val	Ile	Phe	Gly	Asp	Asp	Thr	Asn	Glu	Gly	Thr	Ile	Phe	Val	
				325					330					335		
ccc	aaa	acg	acc	tcc	acc	gtc	ggc	gaa	gcc	gac	acc	ttc	atc	caa	gac	1056
Pro	Lys	Thr	Thr	Ser	Thr	Val	Gly	Glu	Ala	Asp	Thr	Phe	Ile	Gln	Asp	
			340					345					350			
caa	ttc	ccc	aac	atc	aac	ttc	acc	cac	cta	acc	aag	ctg	aac	gac	tgg	1104
Gln	Phe	Pro	Asn	Ile	Asn	Phe	Thr	His	Leu	Thr	Lys	Leu	Asn	Asp	Trp	
		355				360						365				
tat	ctc	aaa	gaa	aac	caa	act	cgc	gag	ttc	ccc	aat	tcc	tcc	ccc	tac	1152
Tyr	Leu	Lys	Glu	Asn	Gln	Thr	Arg	Glu	Phe	Pro	Asn	Ser	Ser	Pro	Tyr	
	370					375					380					
tgg	cgt	ccc	gct	agc	acc	gcg	tac	ggt	gaa	atc	aga	tat	atc	tgt	ccg	1200
Trp	Arg	Pro	Ala	Ser	Thr	Ala	Tyr	Gly	Glu	Ile	Arg	Tyr	Ile	Cys	Pro	
385					390					395					400	
ggg	atc	tac	atg	tcc	tct	gtg	ttt	gct	agt	gcc	ggt	gtc	aac	agc	tgg	1248
Gly	Ile	Tyr	Met	Ser	Ser	Val	Phe	Ala	Ser	Ala	Gly	Val	Asn	Ser	Trp	
				405					410					415		
aac	tat	cat	tat	gct	gtg	cag	gac	ccc	gcc	gcg	gaa	gcc	tca	ggc	aga	1296
Asn	Tyr	His	Tyr	Ala	Val	Gln	Asp	Pro	Ala	Ala	Glu	Ala	Ser	Gly	Arg	
			420					425					430			
ggt	gtc	agt	cat	act	gtg	gaa	gaa	aat	gcc	att	tgg	ggc	ccg	cag	tat	1344
Gly	Val	Ser	His	Thr	Val	Glu	Glu	Asn	Ala	Ile	Trp	Gly	Pro	Gln	Tyr	
		435				440						445				
gtg	agt	ggc	aca	ccg	ccg	gcg	tcg	tat	ctc	act	gag	aat	gcg	cca	att	1392
Val	Ser	Gly	Thr	Pro	Pro	Ala	Ser	Tyr	Leu	Thr	Glu	Asn	Ala	Pro	Ile	
	450					455					460					
gtg	ccg	gtg	atg	cag	ggc	tac	tgg	acg	agt	ttc	att	aga	gtg	ttt	gat	1440
Val	Pro	Val	Met	Gln	Gly	Tyr	Trp	Thr	Ser	Phe	Ile	Arg	Val	Phe	Asp	
465					470					475					480	
ccg	aat	ccg	ctg	agg	tat	ccg	ggg	agt	ccg	gag	tgg	aag	acg	tgg	agt	1488
Pro	Asn	Pro	Leu	Arg	Tyr	Pro	Gly	Ser	Pro	Glu	Trp	Lys	Thr	Trp	Ser	
				485					490					495		
gat	gga	cat	ggg	gag	gat	tat	cgg	cgg	ata	ttt	gtc	cgc	acg	aat	gag	1536
Asp	Gly	His	Gly	Glu	Asp	Tyr	Arg	Arg	Ile	Phe	Val	Arg	Thr	Asn	Glu	
			500					505						510		

21078WO.ST25.txt

acg agg atg gag acg gtg tcg gag gcg cag agg gaa agg tgc gaa tat 1584
 Thr Arg Met Glu Thr Val Ser Glu Ala Gln Arg Glu Arg Cys Glu Tyr
 515 520 525
 tgg agt agt gtt ggg ccg gac ttg tcg cag tga 1617
 Trp Ser Ser Val Gly Pro Asp Leu Ser Gln
 530 535

<210> 30

<211> 538

<212> PRT

<213> *Aspergillus niger*

<400> 30

Met Ile Phe Phe His Leu Ala Pro Phe Phe Phe Leu Phe Gly Leu Val
 1 5 10 15
 Val Ser Ser Gln Asn Pro Thr Val Asp Leu Gly Tyr Thr Arg Tyr Lys
 20 25 30
 Gly Lys Ser Leu Pro Asn Gly Ile Ser Gln Trp Leu Gly Ile Arg Tyr
 35 40 45
 Ala Ala Ala Pro Thr Gly Ser Leu Arg Phe Ser Ala Pro Gln Asp Pro
 50 55 60
 Asp Thr Val Asp Gly Val Gln Glu Ala Phe Lys His Gly Pro Arg Cys
 65 70 75 80
 Val Pro Thr Ser Gln Tyr Pro Thr Pro Ala Gly Thr Ser Glu Asp Cys
 85 90 95
 Leu Phe Leu Asp Val Tyr Ala Pro Ser Ser Val Glu Ala Thr Thr Arg
 100 105 110
 Leu Pro Val Phe Val Trp Ile Gln Gly Gly Gly Phe Asn Ala Asn Ser
 115 120 125
 Ser Pro Asn Tyr Asn Gly Thr Gly Leu Ile Glu Ala Ala Asn Met Ser
 130 135 140
 Met Val Val Val Thr Phe Asn Tyr Arg Val Gly Pro Tyr Gly Phe Leu
 145 150 155 160
 Ser Gly Ser Glu Val Leu Glu Gly Gly Ser Val Asn Asn Gly Leu Lys
 165 170 175
 Asp Gln Ile Lys Val Leu Lys Trp Val Gln Glu His Ile Ser Lys Phe
 180 185 190
 Gly Gly Asp Pro Ser His Val Val Ile Gly Gly Asp Ser Ala Gly Ala
 195 200 205
 Ala Ser Ile Thr Leu His Leu Ser Ala His Gly Gly Arg Asp Asp Glu
 210 215 220
 Leu Phe His Ala Ala Ala Glu Ser Gln Ser Phe Ala Pro Met Leu
 225 230 235 240

21078WO.ST25.txt

Thr Val Asn Gln Ser Gln Phe Ala Tyr Asn Asn Leu Val Ile Arg Ala
 245 250 255
 Gly Cys Ala Ser Asp Ser Asp Thr Leu Ala Cys Leu Arg Arg Leu Asn
 260 265 270
 Thr Thr Glu Leu Gln Arg Ile Asn Ile Asn Thr Pro Leu Pro Thr Ala
 275 280 285
 Gln Gln Ala Pro Leu Tyr Leu Tyr Gly Pro Val Val Asp Gly Ser Leu
 290 295 300
 Ile Pro Asp Tyr Thr Tyr Arg Leu Phe Gln Gln Gly Lys Phe Ile Lys
 305 310 315 320
 Val Pro Val Ile Phe Gly Asp Asp Thr Asn Glu Gly Thr Ile Phe Val
 325 330 335
 Pro Lys Thr Thr Ser Thr Val Gly Glu Ala Asp Thr Phe Ile Gln Asp
 340 345 350
 Gln Phe Pro Asn Ile Asn Phe Thr His Leu Thr Lys Leu Asn Asp Trp
 355 360 365
 Tyr Leu Lys Glu Asn Gln Thr Arg Glu Phe Pro Asn Ser Ser Pro Tyr
 370 375 380
 Trp Arg Pro Ala Ser Thr Ala Tyr Gly Glu Ile Arg Tyr Ile Cys Pro
 385 390 395 400
 Gly Ile Tyr Met Ser Ser Val Phe Ala Ser Ala Gly Val Asn Ser Trp
 405 410 415
 Asn Tyr His Tyr Ala Val Gln Asp Pro Ala Ala Glu Ala Ser Gly Arg
 420 425 430
 Gly Val Ser His Thr Val Glu Glu Asn Ala Ile Trp Gly Pro Gln Tyr
 435 440 445
 Val Ser Gly Thr Pro Pro Ala Ser Tyr Leu Thr Glu Asn Ala Pro Ile
 450 455 460
 Val Pro Val Met Gln Gly Tyr Trp Thr Ser Phe Ile Arg Val Phe Asp
 465 470 475 480
 Pro Asn Pro Leu Arg Tyr Pro Gly Ser Pro Glu Trp Lys Thr Trp Ser
 485 490 495
 Asp Gly His Gly Glu Asp Tyr Arg Arg Ile Phe Val Arg Thr Asn Glu
 500 505 510
 Thr Arg Met Glu Thr Val Ser Glu Ala Gln Arg Glu Arg Cys Glu Tyr
 515 520 525
 Trp Ser Ser Val Gly Pro Asp Leu Ser Gln
 530 535

<210> 31

<211> 4575

<212> DNA

<213> *Aspergillus niger*

21078W0.ST25.txt

<400> 31

gatgcaactt	cagtgaatt	gagacgattg	taactcatca	tcgcatctca	catggaaagg	60
ttgtacaccc	aacaattaga	cctcaacata	tttcacggat	attcctgcaa	gatatataat	120
aaagccatca	ctccactttg	gtagatatgt	tagccaaccg	ggtttgagcg	agtttcttga	180
atggactcat	taagggtagg	atcaattctg	atgtccacaa	ttggctcccta	tttgccagat	240
gtaggcccag	agaattcggg	atcttgacga	tttgcgatgc	tatcccgggt	tccagtaaac	300
tattaggttc	ggctcgggca	caccagacag	acacgactga	cccatgcgct	gccaggaatc	360
ctgataggcc	tagcagtcct	gcgtgcacat	atcggcttgg	tagaaaagga	tagccgtgaa	420
tgtataatct	ttcagatgac	ggttaaatgc	gtttctgtat	ggtgagaagc	tgtgtagatg	480
ggagatgagc	tgtaaattgg	ttcgcagtgg	caacctctag	gctgctgcag	gccggaatac	540
tgcatggcgt	gattttcgtc	gtgaatcttg	ttcatataca	gggtgaaaac	acacgtaagg	600
aaaatcttgt	tatagcaggg	ttgaaaacag	ttgctagaat	tggcagtgc	tgttgcggtt	660
gcaaggggtt	attttgaccc	cttgaagtac	actgcgcttg	gtcaaaggca	aatcacccca	720
tcaagtaata	aatatatatc	tctgttatca	agtcggctcc	tctagtagtg	cagcctcagt	780
acagacaaca	gggactaaca	gcactcttgc	tggtgagctt	gagcgcacct	cacctttctc	840
tccggcctct	ttcgtatttg	gcatttcaat	ggcctgttat	gggacttctg	agcctgcttg	900
attgagtgat	atggtagtgc	gagcgcaaaa	aaggtgattt	tcaaacacca	tgatgcaaag	960
tcagaggtaa	gtgcgagagg	gagatcagga	ggaggagagc	tttatataag	gccgcgtagg	1020
cggcagagac	ggcaagacat	ctggtgaagt	accagcattc	agtgaatttt	ataacagtat	1080
tatttgatcat	cacgactctg	cattgccttt	aataagctcg	gcgtaatttg	gtagggaccc	1140
taggtttgga	tagccccagg	ggggcttggg	gtcgggttg	gagcttgctg	cccagagattc	1200
attttacacc	tagtcaggga	tccgggcggg	ttttatacct	ccctggaggc	ggaatgtacc	1260
tttggttatca	ctgaaaattc	cggccatttt	gttctatttt	actggctatg	gggtttgccca	1320
ctatcgctca	catcctcgca	aggcacctcc	cgatactgca	gtcaaacgtg	ggagttgccg	1380
atagaaacta	caagatcaaa	tctcgttccc	tgggttgagc	ggtcacattc	ggtgaaagag	1440
gtttatcttc	gctccaacca	gcctttcatg	tcgggcgctc	agtgcataag	atccaagcaa	1500
ttttaagcac	tgtactccac	tagtcacact	gttttagcag	tgcatgcttc	tgaatcagga	1560
ctaaactccg	atttttctca	gtgaatactg	ctaaagacaa	ttatgatcct	acagactatc	1620
tctgtgaaaa	agcgcagtta	acttctcgtc	aatcatgaag	ccattttgag	cctttctccg	1680
tcaatcattc	accctactg	ttgactatat	cagccctaag	ggaataaaac	atttgccgta	1740
gaggtgaact	ataactcaat	caatgactga	aagcttaacg	tatctcacia	ttcatctcac	1800
cgtgaagagt	catttacatt	tacgatccag	ccaggccgcg	ctgacatcag	caggcgtgag	1860
agcgcattca	tgcttgctcg	gacataagcc	gaatccattg	catgatgcga	ccttcccga	1920
agagtatggg	tgtccgaact	gaccatgtca	gtggcccat	atggctctca	actacacgaa	1980
cacagacctt	tatcagtccc	ggtccccaca	acttaaattcc	ggagatgcgg	gggtgcagga	2040
atggaacacg	gatacatgtg	tggaatgtag	gaccaaacaa	attggctgtc	gtggacattc	2100
gactcgactt	gacccctcaa	tgcgctggcc	ggaggactga	gccatagggt	ataagaacac	2160
cgtgatcact	catgcctcgt	tatcgctttt	ctatcattat	gtctcgatat	caggaagaca	2220
tagcatgacc	gtgaacacga	tgaagggaat	gctcccgacg	cttagttggg	tggcactggg	2280
catggccagc	ctggcaacct	gcaccaacct	agtagcccag	acaaagaacg	gaagttatta	2340
tggtgtctac	atgcctcagt	ataatgagga	ttattttctt	ggaattccat	ttgctaagcc	2400
cccgttgcca	cacttgcggt	gggccaacct	cgagagtctt	aatgagtctt	ggtcgggatt	2460
gcgccctgct	accggctatg	cgatggtaag	tagcctgaac	agactgctaa	acgacatgt	2520

21078W0.ST25.txt

acttactaac	agcgcgtgtg	ataggaatgt	ataggttacg	gcagtgatca	aaaaggttat	2580
ctgcaggtga	ggatttgacg	ccactttctt	tacgctgttc	tctactaacc	agcaaaatag	2640
agcgaggact	gtctctacct	aaacgtggtc	cgccccgctg	aatacgacaa	tgccagtctt	2700
ccagtccttg	tatggattca	tggtatgtag	tgaaatctac	ctcaacgaca	agttactccc	2760
gacgtgaat	gaacaaaaca	ggcgggtggc	tgcacaagg	cggcactccc	gaccttcgat	2820
acaatcttac	atttattgtt	gaacactcgg	tcaatatcgg	ccagccaatt	atcgcagtga	2880
gcgttgcccta	tcgtctcgg	ccttgggggt	tcttcaatgg	ggtcgagctc	gccaatgagg	2940
gatcgtaaa	tctcgggctg	aaggaccagc	gcttggccct	gcattgggtg	aaagagaaca	3000
ttgcaggttt	cgggtgggtg	tttccataaa	gctattaaac	gtacacagtc	caaaattact	3060
aatgacagtc	actcctatac	aggcgaccct	agtaaagtcg	tgatttacgg	acaaagtgcc	3120
ggctccgaaa	gcgtgggata	ccaaatccgc	gcgtacaacg	gccgagatga	cgggctcttc	3180
cgcgaggagca	tgatggagtc	cggcgcggtg	ttacctggca	gtgccttgaa	cctcacctgg	3240
acatatgagc	cttggttcca	gcaaatagca	gacgaggcag	gatgttccca	gaccaccgcg	3300
aaactggact	gtctacgccg	cacgcccttc	acagtcctaa	acaacattct	gaacaccacc	3360
gccaacgaca	cgacgcctta	caactggagg	cccacagtgg	acggtgactt	cgtagcgcgga	3420
tatcccagcg	agcaactcga	cacaggagac	ttcgtcaaag	taccaatcat	aatcggctac	3480
accacggacg	aaggaacaac	agagtgccca	gaaccagtga	acaccaccgc	cgaattaaaa	3540
gaatacctca	gctgtacgta	cctccttccc	ttcctccctt	atccccccat	ccccatccca	3600
ataacaccaa	cccagcaaca	acaacctacg	gctgggccct	cgactcacag	gtagtatcct	3660
cgctcctgga	cctctacccc	aacaccacct	ccttcggcat	cccatcatcc	gaagaactcg	3720
gcggcaacgt	caccttccca	cagccctacg	gcgccgcatt	ccgccagacg	gcagcatact	3780
acggcgacgc	ccagttcata	gccgcgacgc	gctacacctg	tgagctatgg	gcggcacata	3840
acctgacagc	atattgctac	cgattcaaca	ccaagacaga	cgattacaac	agggagaag	3900
gcgtggcgca	tttctcggac	gtgatcttca	tcttcaacaa	ccttaatgg	tatgggttca	3960
gtccgaaccc	gttcaccaat	gctccagaga	gctatactga	gcttagctac	ctcatgtccg	4020
gctcgtggat	cagcttcaat	aatagtctgg	atcctaataa	gtggactgg	cgcggaagga	4080
acgctacgaa	gacggagaat	tggcccgtgt	atgatctgga	gaatcccttg	agtatgatct	4140
gggatgcaaa	tgctacttcg	tatgcggcgc	cggatacttg	gcgtaaggag	ggtattgcgt	4200
tgattaatgc	taatcggagg	gcgtatcaga	ggtgaatgtg	gtgtagcttg	cagccgttgc	4260
ctacttgttc	gactttcaaa	ctcaaaactt	tctattgaga	gagaaaattg	tgcgaggaaa	4320
gtactaccgc	gggcagaaca	ctctgcgcac	aggtccatat	ctacaaactc	actgaacaga	4380
gtctatagca	gattaggtag	attgtcaagc	ttacatacag	acataacccc	accacaatat	4440
cgtggtaaga	tagcacatct	ctttaaagaa	gaaaaaaaaa	gatgaataca	tataatcggc	4500
tacgtcaata	attcaaaaaca	gaatatgtca	gctgtgcaca	catccgacca	ttacactagt	4560
aaagtgagcg	gcggc					4575

<210> 32

<211> 1695

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

21078W0.ST25.txt

<222> (1)..(1695)

<400> 32

atg aag gga atg ctc ccg acg ctt agt tgg ttg gca ctg ggc atg gcc	48
Met Lys Gly Met Leu Pro Thr Leu Ser Trp Leu Ala Leu Gly Met Ala	
1 5 10 15	
agc ctg gca acc tgc acc aac cca gta gcc cag aca aag aac gga agt	96
Ser Leu Ala Thr Cys Thr Asn Pro Val Ala Gln Thr Lys Asn Gly Ser	
20 25 30	
tat tat ggt gtc tac atg cct cag tat aat gag gat tat ttt ctt gga	144
Tyr Tyr Gly Val Tyr Met Pro Gln Tyr Asn Glu Asp Tyr Phe Leu Gly	
35 40 45	
att cca ttt gct aag ccc ccg ttg gca cac ttg cgt tgg gcc aac ccc	192
Ile Pro Phe Ala Lys Pro Pro Leu Ala His Leu Arg Trp Ala Asn Pro	
50 55 60	
gag agt ctt aat gag tct tgg tcg gga ttg cgc cct gct acc ggc tat	240
Glu Ser Leu Asn Glu Ser Trp Ser Gly Leu Arg Pro Ala Thr Gly Tyr	
65 70 75 80	
gcg atg gaa tgt ata ggt tac ggc agt gat caa aaa ggt tat ctg cag	288
Ala Met Glu Cys Ile Gly Tyr Gly Ser Asp Gln Lys Gly Tyr Leu Gln	
85 90 95	
agc gag gac tgt ctc tac cta aac gtg gtc cgt ccc gct gaa tac gac	336
Ser Glu Asp Cys Leu Tyr Leu Asn Val Val Arg Pro Ala Glu Tyr Asp	
100 105 110	
aat gcc agt ctt cca gtc ctt gta tgg att cat ggc ggt ggc ttc gca	384
Asn Ala Ser Leu Pro Val Leu Val Trp Ile His Gly Gly Gly Phe Ala	
115 120 125	
caa ggc ggc act ccc gac ctt cga tac aat ctt aca ttt att gtt gaa	432
Gln Gly Gly Thr Pro Asp Leu Arg Tyr Asn Leu Thr Phe Ile Val Glu	
130 135 140	
cac tcg gtc aat atc ggc cag cca att atc gca gtg agc gtt gcc tat	480
His Ser Val Asn Ile Gly Gln Pro Ile Ile Ala Val Ser Val Ala Tyr	
145 150 155 160	
cgt ctc ggt cct tgg ggt ttc ttc aat ggg gtc gag ctc gcc aat gag	528
Arg Leu Gly Pro Trp Gly Phe Phe Asn Gly Val Glu Leu Ala Asn Glu	
165 170 175	
gga tcg tta aat ctc ggg ctg aag gac cag cgc ttg gcc ctg cat tgg	576
Gly Ser Leu Asn Leu Gly Leu Lys Asp Gln Arg Leu Ala Leu His Trp	
180 185 190	
gtg aaa gag aac att gca ggt ttc ggt ggc gac cct agt aaa gtc gtg	624
Val Lys Glu Asn Ile Ala Gly Phe Gly Gly Asp Pro Ser Lys Val Val	
195 200 205	
att tac gga caa agt gcc ggc tcc gaa agc gtg gga tac caa atc cgc	672
Ile Tyr Gly Gln Ser Ala Gly Ser Glu Ser Val Gly Tyr Gln Ile Arg	

21078WO.ST25.txt

210	215	220	
gcg tac aac ggc cga gat gac ggg ctc ttc cgc gga ggc atg atg gag			720
Ala Tyr Asn Gly Arg Asp Asp Gly Leu Phe Arg Gly Gly Met Met Glu			
225	230	235	240
tcc ggc gcg gtg tta cct ggc agt gcc ttg aac ctc acc tgg aca tat			768
Ser Gly Ala Val Leu Pro Gly Ser Ala Leu Asn Leu Thr Trp Thr Tyr			
245	250	255	
gag cct tgg ttc cag caa ata gca gac gag gca gga tgt tcc cag acc			816
Glu Pro Trp Phe Gln Gln Ile Ala Asp Glu Ala Gly Cys Ser Gln Thr			
260	265	270	
acc cgc aaa ctg gac tgt cta cgc cgc acg ccc ttc aca gtc cta aac			864
Thr Arg Lys Leu Asp Cys Leu Arg Arg Thr Pro Phe Thr Val Leu Asn			
275	280	285	
aac att ctg aac acc acc gcc aac gac acg acg cct tac aac tgg agg			912
Asn Ile Leu Asn Thr Thr Ala Asn Asp Thr Thr Pro Tyr Asn Trp Arg			
290	295	300	
ccc aca gtg gac ggt gac ttc gta gcg cga tat ccc agc gag caa ctc			960
Pro Thr Val Asp Gly Asp Phe Val Ala Arg Tyr Pro Ser Glu Gln Leu			
305	310	315	320
gac aca gga gac ttc gtc aaa gta cca atc ata atc ggc tac acc acg			1008
Asp Thr Gly Asp Phe Val Lys Val Pro Ile Ile Ile Gly Tyr Thr Thr			
325	330	335	
gac gaa gga aca aca gag tgc cca gaa cca gtg aac acc acc gcc gaa			1056
Asp Glu Gly Thr Thr Glu Cys Pro Glu Pro Val Asn Thr Thr Ala Glu			
340	345	350	
tta aaa gaa tac ctc agc tca aca aca acc tac ggc tgg gcc ctc gac			1104
Leu Lys Glu Tyr Leu Ser Ser Thr Thr Thr Tyr Gly Trp Ala Leu Asp			
355	360	365	
tca cag gta gta tcc tcg ctc ctg gac ctc tac ccc aac acc acc tcc			1152
Ser Gln Val Val Ser Ser Leu Leu Asp Leu Tyr Pro Asn Thr Thr Ser			
370	375	380	
ttc ggc atc cca tca tcc gaa gaa ctc ggc ggc aac gtc acc ttc cca			1200
Phe Gly Ile Pro Ser Ser Glu Glu Leu Gly Gly Asn Val Thr Phe Pro			
385	390	395	400
cag ccc tac ggc gcc gca ttc cgc cag acg gca gca tac tac ggc gac			1248
Gln Pro Tyr Gly Ala Ala Phe Arg Gln Thr Ala Ala Tyr Tyr Gly Asp			
405	410	415	
gcc cag ttc ata gcc gcg acg cgc tac acc tgt gag cta tgg gcg gca			1296
Ala Gln Phe Ile Ala Ala Thr Arg Tyr Thr Cys Glu Leu Trp Ala Ala			
420	425	430	
cat aac ctg aca gca tat tgc tac cga ttc aac acc aag aca gac gat			1344
His Asn Leu Thr Ala Tyr Cys Tyr Arg Phe Asn Thr Lys Thr Asp Asp			
435	440	445	
tac aac agg gaa gaa ggc gtg gcg cat ttc tcg gac gtg atc ttc atc			1392

21078W0.ST25.txt

```

Tyr Asn Arg Glu Glu Gly Val Ala His Phe Ser Asp Val Ile Phe Ile
  450                455                460
ttc aac aac ctt aat ggt tat ggg ttc agt ccg aac ccg ttc acc aat      1440
Phe Asn Asn Leu Asn Gly Tyr Gly Phe Ser Pro Asn Pro Phe Thr Asn
465                470                475                480
gct cca gag agc tat act gag ctt agc tac ctc atg tcc ggc tcg tgg      1488
Ala Pro Glu Ser Tyr Thr Glu Leu Ser Tyr Leu Met Ser Gly Ser Trp
                485                490                495
atc agc ttc act aat agt ctg gat cct aat aag tgg act ggt cgc gga      1536
Ile Ser Phe Thr Asn Ser Leu Asp Pro Asn Lys Trp Thr Gly Arg Gly
                500                505                510
agg aac gct acg aag acg gag aat tgg ccc gtg tat gat ctg gag aat      1584
Arg Asn Ala Thr Lys Thr Glu Asn Trp Pro Val Tyr Asp Leu Glu Asn
                515                520                525
ccc ttg agt atg atc tgg gat gcg aat gtc act tcg tat gcg gcg ccg      1632
Pro Leu Ser Met Ile Trp Asp Ala Asn Val Thr Ser Tyr Ala Ala Pro
                530                535                540
gat act tgg cgt aag gag ggt att gcg ttg att aat gct aat cgg agg      1680
Asp Thr Trp Arg Lys Glu Gly Ile Ala Leu Ile Asn Ala Asn Arg Arg
545                550                555                560
gcg tat cag agg tga      1695
Ala Tyr Gln Arg

```

<210> 33

<211> 564

<212> PRT

<213> *Aspergillus niger*

<400> 33

```

Met Lys Gly Met Leu Pro Thr Leu Ser Trp Leu Ala Leu Gly Met Ala
  1                5                10                15
Ser Leu Ala Thr Cys Thr Asn Pro Val Ala Gln Thr Lys Asn Gly Ser
                20                25                30
Tyr Tyr Gly Val Tyr Met Pro Gln Tyr Asn Glu Asp Tyr Phe Leu Gly
                35                40                45
Ile Pro Phe Ala Lys Pro Pro Leu Ala His Leu Arg Trp Ala Asn Pro
                50                55                60
Glu Ser Leu Asn Glu Ser Trp Ser Gly Leu Arg Pro Ala Thr Gly Tyr
65                70                75                80
Ala Met Glu Cys Ile Gly Tyr Gly Ser Asp Gln Lys Gly Tyr Leu Gln
                85                90                95
Ser Glu Asp Cys Leu Tyr Leu Asn Val Arg Pro Ala Glu Tyr Asp
                100                105                110

```

21078WO.ST25.txt

```

Asn Ala Ser Leu Pro Val Leu Val Trp Ile His Gly Gly Gly Phe Ala
  115                      120                      125
Gln Gly Gly Thr Pro Asp Leu Arg Tyr Asn Leu Thr Phe Ile Val Glu
  130                      135                      140
His Ser Val Asn Ile Gly Gln Pro Ile Ile Ala Val Ser Val Ala Tyr
  145                      150                      155                      160
Arg Leu Gly Pro Trp Gly Phe Phe Asn Gly Val Glu Leu Ala Asn Glu
                      165                      170                      175
Gly Ser Leu Asn Leu Gly Leu Lys Asp Gln Arg Leu Ala Leu His Trp
                      180                      185                      190
Val Lys Glu Asn Ile Ala Gly Phe Gly Gly Asp Pro Ser Lys Val Val
  195                      200                      205
Ile Tyr Gly Gln Ser Ala Gly Ser Glu Ser Val Gly Tyr Gln Ile Arg
  210                      215                      220
Ala Tyr Asn Gly Arg Asp Asp Gly Leu Phe Arg Gly Gly Met Met Glu
  225                      230                      235                      240
Ser Gly Ala Val Leu Pro Gly Ser Ala Leu Asn Leu Thr Trp Thr Tyr
                      245                      250                      255
Glu Pro Trp Phe Gln Gln Ile Ala Asp Glu Ala Gly Cys Ser Gln Thr
  260                      265                      270
Thr Arg Lys Leu Asp Cys Leu Arg Arg Thr Pro Phe Thr Val Leu Asn
  275                      280                      285
Asn Ile Leu Asn Thr Thr Ala Asn Asp Thr Thr Pro Tyr Asn Trp Arg
  290                      295                      300
Pro Thr Val Asp Gly Asp Phe Val Ala Arg Tyr Pro Ser Glu Gln Leu
  305                      310                      315                      320
Asp Thr Gly Asp Phe Val Lys Val Pro Ile Ile Ile Gly Tyr Thr Thr
                      325                      330                      335
Asp Glu Gly Thr Thr Glu Cys Pro Glu Pro Val Asn Thr Thr Ala Glu
  340                      345                      350
Leu Lys Glu Tyr Leu Ser Ser Thr Thr Thr Tyr Gly Trp Ala Leu Asp
  355                      360                      365
Ser Gln Val Val Ser Ser Leu Leu Asp Leu Tyr Pro Asn Thr Thr Ser
  370                      375                      380
Phe Gly Ile Pro Ser Ser Glu Glu Leu Gly Gly Asn Val Thr Phe Pro
  385                      390                      395                      400
Gln Pro Tyr Gly Ala Ala Phe Arg Gln Thr Ala Ala Tyr Tyr Gly Asp
                      405                      410                      415
Ala Gln Phe Ile Ala Ala Thr Arg Tyr Thr Cys Glu Leu Trp Ala Ala
  420                      425                      430
His Asn Leu Thr Ala Tyr Cys Tyr Arg Phe Asn Thr Lys Thr Asp Asp
  435                      440                      445
Tyr Asn Arg Glu Glu Gly Val Ala His Phe Ser Asp Val Ile Phe Ile
  450                      455                      460

```

21078W0.ST25.txt

Phe Asn Asn Leu Asn Gly Tyr Gly Phe Ser Pro Asn Pro Phe Thr Asn
 465 470 475 480
 Ala Pro Glu Ser Tyr Thr Glu Leu Ser Tyr Leu Met Ser Gly Ser Trp
 485 490 495
 Ile Ser Phe Thr Asn Ser Leu Asp Pro Asn Lys Trp Thr Gly Arg Gly
 500 505 510
 Arg Asn Ala Thr Lys Thr Glu Asn Trp Pro Val Tyr Asp Leu Glu Asn
 515 520 525
 Pro Leu Ser Met Ile Trp Asp Ala Asn Val Thr Ser Tyr Ala Ala Pro
 530 535 540
 Asp Thr Trp Arg Lys Glu Gly Ile Ala Leu Ile Asn Ala Asn Arg Arg
 545 550 555 560
 Ala Tyr Gln Arg

<210> 34

<211> 2371

<212> DNA

<213> *Aspergillus niger*

<400> 34

```

gccctgacat ggacggtgtc agatagagac cgttggaagg ctgaaccaca gggcacacgg      60
cacgttgagg accctgcatg ccggtgtatc cggataatgg cagataatcc cggctaattg      120
ggggcgacgg cagctacggc tcacaaattg tgatggaata gacacggcat gatgtttcaa      180
tgaagctcca aactttacag tgctaggctg taaacgtgat tataatcacg atgtaattga      240
ttatcatcta caactcaacc cccgcaccaa gaaatgaatc ctctcgtcgg aagaaaaaga      300
cggcattcca gaagaacttt ttcctagata acaaacagta atcagtccat ccgtccctga      360
cgatcccccc atcgaacctc ggtaagacgc tcgacccaaa aaccagaccg acaagctttt      420
caacctccct aaacgaaaca acggctgtgt tgatcgtgaa cgtgggtgcc tataccaata      480
cgagaaccat ataggataga aattgagttt accgtggaaa agccaccgcg tacagtttaa      540
ttaaccaacc caccacatg cccaaggcac ctgtaacagg gactactgtc cagagagtgg      600
atagtggcta gtgggcagac gtcggatgaa ctccggaaga ccctaactga tacgtagaac      660
catcgtgaac cctggtttgt ccctagtctg gggcgctatt cccagcgtag aaaagcggcc      720
gatcctctga aacagttttc ccccggggta tacttgctag ttagtcacta tcatacaaaa      780
gtagtgtagt ggacaagacc aggttctact actattagtt agttctgttt catcccgact      840
caattttgcg tccaagacc ctgggttgtc cgggcctgtc ttgcccaaca cgagatgtat      900
ggagtaagta tggagggaga ctaacctcgg aatattcttg tctcttttta gtactatcta      960
gcccttagtg agactatagc agtagtgaa cagagagaga gagagatgtc tatataagta      1020
cagtcgtaga tccctaaaca tgaccagctt cagactcaga ctcgagcagc cagtgcagtc      1080
cagtcactc tttcattctc accccttctt tactatctta caataatttc tattcaataa      1140
gtctgcagtg cagcaccac acacattcat tctctgagag ataaaaaata acaaaatggc      1200
ccccctcaaa tccctcctcc tcggcgccct cctggccacc ctcgcccttt ccacccact      1260
ggcaaccgac gccgaaaacc tctacgcacg tcaattcggc acgggctcta cagccaacga      1320
actcgagcag ggaagctgca aggatgtgac tctcatcttt gcgagggggg caactgagct      1380

```

21078W0.ST25.txt

tggaatatg	gtatgcttgt	tgctgcctt	taccgtact	atactatccc	agaacatacc	1440
aagcacaaca	tcacaaaaca	tgtggagcca	ggagctaata	agtgggtggtg	atgatatgat	1500
gtagggcacc	gtaatcggcc	cccctctctg	cgacaacctg	aaatccaaac	tcggatccga	1560
caaagtcgcc	tgccaggggtg	tcggcggcca	atacagcgcc	ggactcgtgc	agaatgccct	1620
gccccagAAC	accgatccgg	ggagtatctc	cgccgcgaag	cagatgttcg	aggaggcgaa	1680
ttcgaagtgt	cccaatacta	agattgttgc	gggtggttat	aggtatatat	ccctttcccc	1740
tttaccttcc	cccatatcaa	tgctagaggc	aaaggaatat	catgctaata	tagatgttgg	1800
ggaaacagtc	aaggaagcgc	tgtgattgac	aacgccgtgc	aagaactcag	caccaccgtg	1860
aaagaccaag	tgaagggtgt	cgtgctcttc	gggttcacga	gaaacgtgca	ggatcacggg	1920
cagatcccta	attaccctaa	ggatgacgtg	aaggtttatt	gtgccgtggg	cgatctggtc	1980
tgtgatgata	cgttggttgt	tacggcgatg	catctgacgt	atggcatgga	tgcgggtgat	2040
gcggcgagct	ttttggccga	gaaggtgcag	tcttcagta	gttcgactac	tagctccagc	2100
tcggatgccg	cgagtagttc	atctgctgcg	gggacgtcgt	cgtcgggggtt	gtcggggactg	2160
tcttcttttt	ttggaggctt	ctaaatagaa	ttagatgaga	tgagtgggtcc	gggtgggggt	2220
ttaggggatt	gttgttcggt	tctcttggtg	gatttagttt	ccgttatatta	cttagctggg	2280
ataagatata	tggtacatag	tatagatgtg	ttgtgatgtt	attctggcta	ttttgtacac	2340
tttgacatga	tctgcgatat	gggagcgtct	a			2371

<210> 35

<211> 789

<212> DNA

<213> *Aspergillus niger*

<220>

<221> CDS

<222> (1)..(789)

<400> 35

atg gcc ccc ctc aaa tcc ctc ctc ctc ggc gcc tcc ctg gcc acc ctc	48
Met Ala Pro Leu Lys Ser Leu Leu Leu Gly Ala Ser Leu Ala Thr Leu	
1 5 10 15	
gcc ctt tcc acc cca ctg gca acc gac gcc gaa aac ctc tac gca cgt	96
Ala Leu Ser Thr Pro Leu Ala Thr Asp Ala Glu Asn Leu Tyr Ala Arg	
20 25 30	
caa ttc ggc acg ggc tct aca gcc aac gaa ctc gag cag gga agc tgc	144
Gln Phe Gly Thr Gly Ser Thr Ala Asn Glu Leu Glu Gln Gly Ser Cys	
35 40 45	
aag gat gtg act ctc atc ttt gcg agg ggg tca act gag ctt ggg aat	192
Lys Asp Val Thr Leu Ile Phe Ala Arg Gly Ser Thr Glu Leu Gly Asn	
50 55 60	
atg ggc acc gta atc ggc ccc cct ctc tgc gac aac ctg aaa tcc aaa	240
Met Gly Thr Val Ile Gly Pro Pro Leu Cys Asp Asn Leu Lys Ser Lys	
65 70 75 80	

21078W0.ST25.txt

```

ctc gga tcc gac aaa gtc gcc tgc cag ggt gtc ggc ggc caa tac agc      288
Leu Gly Ser Asp Lys Val Ala Cys Gln Gly Val Gly Gly Gln Tyr Ser
      85                      90                      95
gcc gga ctc gtg cag aat gcc ctg ccc cag aac acc gat ccg ggg agt      336
Ala Gly Leu Val Gln Asn Ala Leu Pro Gln Asn Thr Asp Pro Gly Ser
      100                    105                    110
atc tcc gcc gcg aag cag atg ttc gag gag gcg aat tcg aag tgt ccc      384
Ile Ser Ala Ala Lys Gln Met Phe Glu Glu Ala Asn Ser Lys Cys Pro
      115                    120                    125
aat act aag att gtt gcg ggt ggt tat agt caa gga agc gct gtg att      432
Asn Thr Lys Ile Val Ala Gly Gly Tyr Ser Gln Gly Ser Ala Val Ile
      130                    135                    140
gac aac gcc gtg caa gaa ctc agc acc acc gtg aaa gac caa gtg aag      480
Asp Asn Ala Val Gln Glu Leu Ser Thr Thr Val Lys Asp Gln Val Lys
      145                    150                    155                    160
ggg gtc gtg ctc ttc ggg ttc acg aga aac gtg cag gat cac ggg cag      528
Gly Val Val Leu Phe Gly Phe Thr Arg Asn Val Gln Asp His Gly Gln
      165                    170                    175
atc cct aat tac cct aag gat gac gtg aag gtt tat tgt gcc gtg ggc      576
Ile Pro Asn Tyr Pro Lys Asp Asp Val Lys Val Tyr Cys Ala Val Gly
      180                    185                    190
gat ctg gtc tgt gat gat acg ttg gtt gtt acg gcg atg cat ctg acg      624
Asp Leu Val Cys Asp Asp Thr Leu Val Val Thr Ala Met His Leu Thr
      195                    200                    205
tat ggc atg gat gcg ggt gat gcg gcg agc ttt ttg gcc gag aag gtg      672
Tyr Gly Met Asp Ala Gly Asp Ala Ala Ser Phe Leu Ala Glu Lys Val
      210                    215                    220
cag tct tcc agt agt tcg act act agc tcc agc tcg gat gcc gcg agt      720
Gln Ser Ser Ser Ser Ser Thr Thr Ser Ser Ser Ser Asp Ala Ala Ser
      225                    230                    235                    240
agt tca tct gct gcg ggg acg tcg tcg tcg ggg ttg tcg gga ctg tct      768
Ser Ser Ser Ala Ala Gly Thr Ser Ser Ser Gly Leu Ser Gly Leu Ser
      245                    250                    255
tct ttt ttt gga ggt ctc taa      789
Ser Phe Phe Gly Gly Leu
      260

```

<210> 36

<211> 262

<212> PRT

<213> Aspergillus niger

<400> 36

21078W0.ST25.txt

Met Ala Pro Leu Lys Ser Leu Leu Leu Gly Ala Ser Leu Ala Thr Leu
 1 5 10 15
 Ala Leu Ser Thr Pro Leu Ala Thr Asp Ala Glu Asn Leu Tyr Ala Arg
 20 25 30
 Gln Phe Gly Thr Gly Ser Thr Ala Asn Glu Leu Glu Gln Gly Ser Cys
 35 40 45
 Lys Asp Val Thr Leu Ile Phe Ala Arg Gly Ser Thr Glu Leu Gly Asn
 50 55 60
 Met Gly Thr Val Ile Gly Pro Pro Leu Cys Asp Asn Leu Lys Ser Lys
 65 70 75 80
 Leu Gly Ser Asp Lys Val Ala Cys Gln Gly Val Gly Gly Gln Tyr Ser
 85 90 95
 Ala Gly Leu Val Gln Asn Ala Leu Pro Gln Asn Thr Asp Pro Gly Ser
 100 105 110
 Ile Ser Ala Ala Lys Gln Met Phe Glu Glu Ala Asn Ser Lys Cys Pro
 115 120 125
 Asn Thr Lys Ile Val Ala Gly Gly Tyr Ser Gln Gly Ser Ala Val Ile
 130 135 140
 Asp Asn Ala Val Gln Glu Leu Ser Thr Thr Val Lys Asp Gln Val Lys
 145 150 155 160
 Gly Val Val Leu Phe Gly Phe Thr Arg Asn Val Gln Asp His Gly Gln
 165 170 175
 Ile Pro Asn Tyr Pro Lys Asp Asp Val Lys Val Tyr Cys Ala Val Gly
 180 185 190
 Asp Leu Val Cys Asp Asp Thr Leu Val Val Thr Ala Met His Leu Thr
 195 200 205
 Tyr Gly Met Asp Ala Gly Asp Ala Ala Ser Phe Leu Ala Glu Lys Val
 210 215 220
 Gln Ser Ser Ser Ser Ser Thr Thr Ser Ser Ser Ser Asp Ala Ala Ser
 225 230 235 240
 Ser Ser Ser Ala Ala Gly Thr Ser Ser Ser Gly Leu Ser Gly Leu Ser
 245 250 255
 Ser Phe Phe Gly Gly Leu
 260

<210> 37

<211> 2981

<212> DNA

<213> *Aspergillus niger*

<400> 37

tcctcatccc atgctctccc ggcagaaccc cggagacaac ccacactaat gcacccaaag 60
 caaaatgaca tggattgaat tatccggggt gcatccatct tggtccccca cacattggac 120

21078WO.ST25.txt

cctttcctta	taatggctgc	cccggcaaac	ccccaatgct	tgtttaggcc	agcgagata	180
gcaaattctct	cgtctgatta	acgatgctaa	agctcgctgt	tgctcttttt	tcgttacttg	240
ccgtgggcaa	tgcagcgcca	accaaagtgg	cccgttcac	ggccagtcct	acggccaagg	300
ttcgcaacgg	tacatatgtc	ggagtgacaa	atgcgcatta	ccagcaagat	ttcttttttg	360
gaatgccgta	tgcccagcag	ccttttaggtg	acttgcgctt	cacggtgcct	cagtccctga	420
acgaaagctg	gagtggcgag	cgcgacgcga	aggaatatct	caatatctgt	gtaggatacg	480
gtgtgagtgc	gcaaattctt	ttcgagagcc	aggccctact	agctgcatcc	tggcactatg	540
aataataatct	aatgggtaga	tctgttagac	cgactcgatt	tggtaccac	agtccgaagc	600
ttgtctaacc	ttgaatgtca	tccgcgattc	ttctgcaaat	gagaactcga	agctccccgt	660
ggcgctctgg	atacatggag	gtggcttctt	tgagggatct	agtgtgacc	agcgctacaa	720
catgtccgcg	attgttgcca	actcctataa	gatcggtatg	tcgacgtatg	cggttgtaga	780
attagactga	ctcggttgc	tcgcattgta	ggaaagccgt	tcattgctgt	cagcttaaac	840
tatcgccttt	cggcatgggg	cttcttgagt	tccagtcaag	tctggggcac	tggcaatacc	900
aatctaggta	tcagggatca	aaggtttagca	ctccattgga	tcaaggagaa	tatcgcggca	960
ttcggaggag	acccagataa	gatcactatc	tggggcgaat	ctgccggagc	gatgtccgtg	1020
ggttatcacc	ttgcagcata	cggcggtagg	gacgatggac	tcttccgtgg	aggaattatg	1080
gagtcaggag	ggactattgc	agctagtcca	gccaactata	ccgggtacca	agcgactat	1140
gatgagctcg	cgggtcaagt	cggttgctcc	gacgtagtag	attcgttgca	gtgcctgcgc	1200
gaagttccgt	tcgagaaatt	gaacgctgct	ctcaacacca	ccagtggtaa	ctcggatttc	1260
aatttcgggc	ccgtcattga	tggagatata	atcagggact	ggggcagcct	ccagctagac	1320
aagcatgaat	tcgtcaaagt	ccctattctt	gcaggtagca	ataccgacga	agggacagcc	1380
tttgggcca	caggatcaaa	cacgacagag	gagttctatg	catatctcac	aggatgtgt	1440
gataatgagt	taacatcctg	aaagaacccc	agagcagcaa	aacgggctaa	tctcactggc	1500
agatggcgaa	tctggattcc	agctaccccc	cacgatcgcc	caggaaatcc	tgcagctcta	1560
ccctgatgat	ccagcactgg	gcacccccga	atttctcggg	gacactagag	tcccgtccaa	1620
aggctaccaa	tggcggcgca	cctgtgcata	cgcaggggac	tatgtaatgc	atgccaaccg	1680
tcgccgacaa	tgtgaggcgt	ggacagagac	ctcgacgacg	gcgtactgtt	atcgattcaa	1740
tatgcgtgcg	gccgatgtcc	ccatcctgtc	tggcgccacc	cattttgaag	aagttgcttt	1800
tgtattcaac	aacattgcag	gactcgggta	ccattacgga	aagccgttcg	cagggatgcc	1860
cgagtcctac	gtacagctaa	gcaacttgat	gaccagcatg	tgggcaccc	tcacccacga	1920
tttagaccct	aatttcgggca	tcaaggactc	agctgtacag	tggcaaccgt	acgggaagga	1980
tcagccggtt	gatctagtgt	ttgatgcgaa	tgtcacgagc	tacagctaca	tggagccaga	2040
cacgtggcgg	aaggagggga	tcgactatat	caattccgtg	gccaacgcgt	actggcgata	2100
agcttcatgc	tatcgaaaac	acatgtgatg	agcgtgagag	tttttgccct	ccgcttgatg	2160
ttgcctgcga	gaggaaaagg	ttaaggcaaa	caaggatggg	agggggtgcg	agcgcatcta	2220
agtcggccac	ggtagttagt	tgatggttcc	ctcgttagaa	gcaaatacag	atgccatact	2280
tcctgcaaca	aaccagaac	ttgttgtaat	caagtttttt	caaacggatg	gtagatcggt	2340
tccgatttgt	aaaaagcaag	atcctagcgt	tacgagggaa	ccaagacacc	cacacagagg	2400
agcattacga	attccaaatt	accaaagcct	gtataacaaa	aaccagcaga	gaccgcctaa	2460
ttagtcaact	acagcattgg	ttcaatgtac	ctgcaaggac	ctttacacgc	gtggtcaccc	2520
atgtaccaag	ccaagccaac	ggccaagaca	cggaaataac	caagaggaaa	ccactccctc	2580
caagaatcaa	gaaccaggg	ggtcaagaga	atctggaagc	gataaagggg	tcttcttttt	2640
tttctttgct	tacctagaga	gggaggagtc	ggcgttcatc	gtcaatcagt	agagtgttct	2700
ccgccctgag	tggtgtagtc	tatatccgga	ccatcgggga	catgattatc	atacgatcca	2760

21078W0.ST25.txt

taaccaagtc cccgattgta ctacggctac caaaactaga atgatgaaaa tattggagta	2820
cgaaaggaac taaaccaata ctaagaaaaa aaaaaaagag taaagaaaaa agagtaaaaa	2880
accaagctcg gaaagtaaaa atttcccctg gtcttgttgt cattccccta cctattgaga	2940
accgggttca ccaatgacag cggatccccg atttgacatc g	2981

<210> 38

<211> 1686

<212> DNA

<213> Aspergillus niger

<220>

<221> CDS

<222> (1)..(1686)

<400> 38

atg cta aag ctc gct gtt gct ctt ttt tcg tta ctt gcc gtg ggc aat	48
Met Leu Lys Leu Ala Val Ala Leu Phe Ser Leu Leu Ala Val Gly Asn	
1 5 10 15	
gca gcg cca acc aaa gtg gcc cgt tcc acg gcc agt cct acg gcc aag	96
Ala Ala Pro Thr Lys Val Ala Arg Ser Thr Ala Ser Pro Thr Ala Lys	
20 25 30	
gtt cgc aac ggt aca tat gtc gga gtg aca aat gcg cat tac cag caa	144
Val Arg Asn Gly Thr Tyr Val Gly Val Thr Asn Ala His Tyr Gln Gln	
35 40 45	
gat ttc ttt ttg gga atg ccg tat gcc cag cag cct tta ggt gac ttg	192
Asp Phe Phe Leu Gly Met Pro Tyr Ala Gln Gln Pro Leu Gly Asp Leu	
50 55 60	
cgc ttc acg gtg cct cag tcc ctg aac gaa agc tgg agt ggc gag cgc	240
Arg Phe Thr Val Pro Gln Ser Leu Asn Glu Ser Trp Ser Gly Glu Arg	
65 70 75 80	
gac gcg aag gaa tat tcc aat atc tgt gta gga tac ggt acc gac tcg	288
Asp Ala Lys Glu Tyr Ser Asn Ile Cys Val Gly Tyr Gly Thr Asp Ser	
85 90 95	
att tgg tac cca cag tcc gaa gct tgt cta acc ttg aat gtc atc cgc	336
Ile Trp Tyr Pro Gln Ser Glu Ala Cys Leu Thr Leu Asn Val Ile Arg	
100 105 110	
gat tct tct gca aat gag aac tcg aag ctc ccc gtg ggc gtc tgg ata	384
Asp Ser Ser Ala Asn Glu Asn Ser Lys Leu Pro Val Gly Val Trp Ile	
115 120 125	
cat gga ggt ggc ttc ttt gag gga tct agt gct gac cag cgc tac aac	432
His Gly Gly Gly Phe Phe Glu Gly Ser Ser Ala Asp Gln Arg Tyr Asn	
130 135 140	
atg tcc gcg att gtt gcc aac tcc tat aag atc gga aag ccg ttc att	480

21078W0.ST25.txt

Met Ser Ala Ile Val Ala Asn Ser Tyr Lys Ile Gly Lys Pro Phe Ile	
145 150 155 160	
gct gtc agc tta aac tat cgc ctt tcg gca tgg ggc ttc ttg agt tcc	528
Ala Val Ser Leu Asn Tyr Arg Leu Ser Ala Trp Gly Phe Leu Ser Ser	
165 170 175	
agt caa gtc tgg ggc act ggc aat acc aat cta ggt atc agg gat caa	576
Ser Gln Val Trp Gly Thr Gly Asn Thr Asn Leu Gly Ile Arg Asp Gln	
180 185 190	
agg tta gca ctc cat tgg atc aag gag aat atc gcg gca ttc gga gga	624
Arg Leu Ala Leu His Trp Ile Lys Glu Asn Ile Ala Ala Phe Gly Gly	
195 200 205	
gac cca gat aag atc act atc tgg ggc gaa tct gcc gga gcg atg tcc	672
Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser Ala Gly Ala Met Ser	
210 215 220	
gtg ggt tat cac ctt gca gca tac ggc ggt agg gac gat gga ctc ttc	720
Val Gly Tyr His Leu Ala Ala Tyr Gly Gly Arg Asp Asp Gly Leu Phe	
225 230 235 240	
cgt gga gga att atg gag tca gga ggg act att gca gct agt cca gcc	768
Arg Gly Gly Ile Met Glu Ser Gly Gly Thr Ile Ala Ala Ser Pro Ala	
245 250 255	
aac tat acc ggg tac caa gcg cac tat gat gag ctc gcg ggt caa gtc	816
Asn Tyr Thr Gly Tyr Gln Ala His Tyr Asp Glu Leu Ala Gly Gln Val	
260 265 270	
ggt tgc tcc gac gta gta gat tcg ttg cag tgc ctg cgc gaa gtt ccg	864
Gly Cys Ser Asp Val Val Asp Ser Leu Gln Cys Leu Arg Glu Val Pro	
275 280 285	
ttc gag aaa ttg aac gct gct ctc aac acc acc agt ggt aac tcg gat	912
Phe Glu Lys Leu Asn Ala Ala Leu Asn Thr Thr Ser Gly Asn Ser Asp	
290 295 300	
ttc aat ttc ggg ccc gtc att gat gga gat ata atc agg gac tgg ggc	960
Phe Asn Phe Gly Pro Val Ile Asp Gly Asp Ile Ile Arg Asp Trp Gly	
305 310 315 320	
agc ctc cag cta gac aag cat gaa ttc gtc aaa gtc cct att ctt gca	1008
Ser Leu Gln Leu Asp Lys His Glu Phe Val Lys Val Pro Ile Leu Ala	
325 330 335	
ggt acc aat acc gac gaa ggg aca gcc ttt ggg ccc aca ggt atc aac	1056
Gly Thr Asn Thr Asp Glu Gly Thr Ala Phe Gly Pro Thr Gly Ile Asn	
340 345 350	
acg aca gag gag ttc tat gca tat ctc aca gat ggc gaa tct gga ttc	1104
Thr Thr Glu Glu Phe Tyr Ala Tyr Leu Thr Asp Gly Glu Ser Gly Phe	
355 360 365	
cag cta ccc ccc acg atc gcc cag gaa atc ctg cag ctc tac cct gat	1152
Gln Leu Pro Pro Thr Ile Ala Gln Glu Ile Leu Gln Leu Tyr Pro Asp	
370 375 380	

21078W0.ST25.txt

```

gat cca gca ctg ggc atc ccc gaa ttt ctc ggt gac act aga gtc ccg      1200
Asp Pro Ala Leu Gly Ile Pro Glu Phe Leu Gly Asp Thr Arg Val Pro
385          390 .          395          400
tcc aaa ggc tac caa tgg cgg cgc acc tgt gca tac gca ggg gac tat      1248
Ser Lys Gly Tyr Gln Trp Arg Arg Thr Cys Ala Tyr Ala Gly Asp Tyr
          405          410          415
gta atg cat gcc aac cgt cgc cga caa tgt gag gcg tgg aca gag acc      1296
Val Met His Ala Asn Arg Arg Arg Gln Cys Glu Ala Trp Thr Glu Thr
          420          425          430
tcg acg acg gcg tac tgt tat cga ttc aat atg cgt gcg gcc gat gtc      1344
Ser Thr Thr Ala Tyr Cys Tyr Arg Phe Asn Met Arg Ala Ala Asp Val
          435          440          445
ccc atc ctg tct ggc gcc acc cat ttt gaa gaa gtt gct ttt gta ttc      1392
Pro Ile Leu Ser Gly Ala Thr His Phe Glu Glu Val Ala Phe Val Phe
          450          455          460
aac aac att gca gga ctc ggg tac cat tac gga aag ccg ttc gca ggg      1440
Asn Asn Ile Ala Gly Leu Gly Tyr His Tyr Gly Lys Pro Phe Ala Gly
465          470          475          480
atg ccc gag tcc tac gta cag cta agc aac ttg atg acc agc atg tgg      1488
Met Pro Glu Ser Tyr Val Gln Leu Ser Asn Leu Met Thr Ser Met Trp
          485          490          495
gca tcc ttc atc cac gat tta gac cct aat tcg ggc atc aag gac tca      1536
Ala Ser Phe Ile His Asp Leu Asp Pro Asn Ser Gly Ile Lys Asp Ser
          500          505          510
gct gta cag tgg caa ccg tac ggg aag gat cag ccg gtt gat cta gtg      1584
Ala Val Gln Trp Gln Pro Tyr Gly Lys Asp Gln Pro Val Asp Leu Val
          515          520          525
ttt gat gcg aat gtc acg agc tac agc tac atg gag cca gac acg tgg      1632
Phe Asp Ala Asn Val Thr Ser Tyr Ser Tyr Met Glu Pro Asp Thr Trp
          530          535          540
cgg aag gag ggg atc gac tat atc aat tcc gtg gcc aac gcg tac tgg      1680
Arg Lys Glu Gly Ile Asp Tyr Ile Asn Ser Val Ala Asn Ala Tyr Trp
545          550          555          560
cga taa
Arg
1686

```

<210> 39

<211> 561

<212> PRT

<213> *Aspergillus niger*

<400> 39

Met Leu Lys Leu Ala Val Ala Leu Phe Ser Leu Leu Ala Val Gly Asn

21078W0.ST25.txt

1	5	10	15
Ala Ala Pro Thr Lys Val Ala Arg Ser Thr Ala Ser Pro Thr Ala Lys			
20	25	30	
Val Arg Asn Gly Thr Tyr Val Gly Val Thr Asn Ala His Tyr Gln Gln			
35	40	45	
Asp Phe Phe Leu Gly Met Pro Tyr Ala Gln Gln Pro Leu Gly Asp Leu			
50	55	60	
Arg Phe Thr Val Pro Gln Ser Leu Asn Glu Ser Trp Ser Gly Glu Arg			
65	70	75	80
Asp Ala Lys Glu Tyr Ser Asn Ile Cys Val Gly Tyr Gly Thr Asp Ser			
85	90	95	
Ile Trp Tyr Pro Gln Ser Glu Ala Cys Leu Thr Leu Asn Val Ile Arg			
100	105	110	
Asp Ser Ser Ala Asn Glu Asn Ser Lys Leu Pro Val Gly Val Trp Ile			
115	120	125	
His Gly Gly Gly Phe Phe Glu Gly Ser Ser Ala Asp Gln Arg Tyr Asn			
130	135	140	
Met Ser Ala Ile Val Ala Asn Ser Tyr Lys Ile Gly Lys Pro Phe Ile			
145	150	155	160
Ala Val Ser Leu Asn Tyr Arg Leu Ser Ala Trp Gly Phe Leu Ser Ser			
165	170	175	
Ser Gln Val Trp Gly Thr Gly Asn Thr Asn Leu Gly Ile Arg Asp Gln			
180	185	190	
Arg Leu Ala Leu His Trp Ile Lys Glu Asn Ile Ala Ala Phe Gly Gly			
195	200	205	
Asp Pro Asp Lys Ile Thr Ile Trp Gly Glu Ser Ala Gly Ala Met Ser			
210	215	220	
Val Gly Tyr His Leu Ala Ala Tyr Gly Gly Arg Asp Asp Gly Leu Phe			
225	230	235	240
Arg Gly Gly Ile Met Glu Ser Gly Gly Thr Ile Ala Ala Ser Pro Ala			
245	250	255	
Asn Tyr Thr Gly Tyr Gln Ala His Tyr Asp Glu Leu Ala Gly Gln Val			
260	265	270	
Gly Cys Ser Asp Val Val Asp Ser Leu Gln Cys Leu Arg Glu Val Pro			
275	280	285	
Phe Glu Lys Leu Asn Ala Ala Leu Asn Thr Thr Ser Gly Asn Ser Asp			
290	295	300	
Phe Asn Phe Gly Pro Val Ile Asp Gly Asp Ile Ile Arg Asp Trp Gly			
305	310	315	320
Ser Leu Gln Leu Asp Lys His Glu Phe Val Lys Val Pro Ile Leu Ala			
325	330	335	
Gly Thr Asn Thr Asp Glu Gly Thr Ala Phe Gly Pro Thr Gly Ile Asn			
340	345	350	
Thr Thr Glu Glu Phe Tyr Ala Tyr Leu Thr Asp Gly Glu Ser Gly Phe			

21078WO.ST25.txt

355	360	365
Gln Leu Pro Pro Thr Ile Ala Gln Glu Ile Leu Gln Leu Tyr Pro Asp		
370	375	380
Asp Pro Ala Leu Gly Ile Pro Glu Phe Leu Gly Asp Thr Arg Val Pro		
385	390	395
Ser Lys Gly Tyr Gln Trp Arg Arg Thr Cys Ala Tyr Ala Gly Asp Tyr		
405	410	415
Val Met His Ala Asn Arg Arg Arg Gln Cys Glu Ala Trp Thr Glu Thr		
420	425	430
Ser Thr Thr Ala Tyr Cys Tyr Arg Phe Asn Met Arg Ala Ala Asp Val		
435	440	445
Pro Ile Leu Ser Gly Ala Thr His Phe Glu Glu Val Ala Phe Val Phe		
450	455	460
Asn Asn Ile Ala Gly Leu Gly Tyr His Tyr Gly Lys Pro Phe Ala Gly		
465	470	475
Met Pro Glu Ser Tyr Val Gln Leu Ser Asn Leu Met Thr Ser Met Trp		
485	490	495
Ala Ser Phe Ile His Asp Leu Asp Pro Asn Ser Gly Ile Lys Asp Ser		
500	505	510
Ala Val Gln Trp Gln Pro Tyr Gly Lys Asp Gln Pro Val Asp Leu Val		
515	520	525
Phe Asp Ala Asn Val Thr Ser Tyr Ser Tyr Met Glu Pro Asp Thr Trp		
530	535	540
Arg Lys Glu Gly Ile Asp Tyr Ile Asn Ser Val Ala Asn Ala Tyr Trp		
545	550	555
Arg		560